

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 06:47:29 ; Search time 8799 Seconds
(without alignments)
7873.651 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 agggtccttagccgggcgc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	ID	
	1	1180.4	50.9	1182	29	AY404343 Homo sapi
	2	912.2	39.3	2197	11	AK050128 Mus muscu
	3	857.4	37.0	1180	29	AY404344 Pan trogl
	4	853.2	36.8	879	13	BQ216829 AGENCOURT
	5	738	31.8	916	14	CD050395 AGENCOURT
	6	733.8	31.6	1185	29	AY404345 Mus muscu
	7	731.6	31.5	1353	11	AK041045 Mus muscu
	8	522.4	22.5	978	12	BI102968 602888578
	9	488.6	21.1	761	12	BI559553 603252894
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c	11	457.6	19.7	659	14	CB435346 615435 MA
	12	452.6	19.5	1723	11	AK052644 Mus muscu
	13	450	19.4	724	14	CB952493 AGENCOURT
	14	444.4	19.2	481	14	CB158774 K-EST0218
c	15	442	19.1	583	9	AI694348 wd45g04.x
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c	17	435.8	18.8	439	9	AA633698 ag87a11.s
	18	431.6	18.6	899	12	BI246549 602958449
c	19	430	18.5	430	9	AI917116 ts52a02.x
c	20	422	18.2	422	9	AI580389 tm42f08.x
c	21	417	18.0	1055	9	AI654867 wb65c12.x
	22	415.8	17.9	660	10	BB221592 BB221592
c	23	410.2	17.7	478	9	AI015041 ov51a05.s
	24	406.4	17.5	901	12	BI827790 603075472
	25	404.8	17.4	1021	14	CK231266 ILLUMIGEN
c	26	400	17.2	543	10	AW236852 xm49h11.x
	27	396.4	17.1	721	12	BG972539 602841125
c	28	393.4	17.0	470	9	AA974327 oq10g06.s
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	31	387.8	16.7	738	14	CB954127 AGENCOURT
	32	386.6	16.7	751	28	AQ748070 HS_5538_A
	33	384.8	16.6	886	12	BI101074 602886333
c	34	384.6	16.6	454	9	AA970255 op64h06.s
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	42	368.4	15.9	763	14	CD241803 AGENCOURT
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	44	361.6	15.6	1193	12	BI102573 602889579
c	45	357	15.4	363	14	Z39483 HSC1BC022 n

ALIGNMENTS

RESULT 1
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 LOCUS AY404343 1182 bp DNA linear GSS 12-DEC-2003
 DEFINITION Homo sapiens HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY404343
 VERSION AY404343.1 GI:39760320
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1182)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1182)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES Location/Qualifiers
 source 1. .1182
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 /db_xref="taxon:9606"
 gene <1. .>1182
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 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 458 ATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGT 517
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 Db 1 ATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGT 60
 Qy 518 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTC 577
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Qy	578	GGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTG	637
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Qy	638	CTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTC	697
Db	181	CTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTC	240
Qy	698	TGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTTACA	757
Db	241	TGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTTACA	300
Qy	758	GAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAC	817
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Qy	818	TCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGC	877
Db	361	TCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGC	420
Qy	878	TTGATGGAAAAACCTATTAACCAGTACCACAAGACTTGGAGAAC TTCATTGCCAAGTTT	937
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Qy	1238	TTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATT	1297
Db	781	TTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATT	840
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Db	841	CAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGAC	900
Qy	1358	AAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGC	1417
Db	901	AAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGC	960
Qy	1418	CCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCAC	1477

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Qy      1538 TTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCT 1597
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Qy      1598 GTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAA 1639
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Db      1141 GTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAA 1182

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RESULT 2

AK050128

LOCUS AK050128 2197 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730018P11 product:hypothetical UDP-glucoronosyl and UDP-glucosyl transferase containing protein, full insert sequence.

ACCESSION AK050128

VERSION AK050128.1 GI:26340835

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2197)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .2197

/organism="Mus musculus"

/mol_type="mRNA"

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/db_xref="taxon:10090"

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Matches 1201;  Conservative 0;  Mismatches 438;  Indels 6;  Gaps 2;

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Db      32 AGGGTCCCTTAGTGGGGCACAGCTCTTTAGGTGTGCAACCTGTGTCAGGGCTCCACATAT 91

Qy      61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
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Db      92 TCTACAGATGGCAGCACATCGGCGTTGGCTTCTCATGAGCTTCCTTTTCTTGGAGTTAT 151

Qy      121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Qy      181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACCATGCTTAACCA 240
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Qy      361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
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Db	1229	GGCTGTCCATCATGGAGTACCATGGTGGGGATCCATTTTTTTTTTGACCAACCTGAAAA	1288
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Qy	1318	AGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGC	1377
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Qy	1378	AGTGGCTGCCAGTGTCTCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGG	1437
Db	1409	AATGGCCTCCAAGATTATCAGGCACTCCACCCACTGACCCCTGCCAGAGGCTTTTGGG	1468
Qy	1438	CTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCA	1497
Db	1469	CTGGATAGATCATATCTTGACAGACAGGGGGTGCAGCACATCTCAAGCCATATGCTTTCCA	1528
Qy	1498	GCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCT	1557
Db	1529	GCAGCCATGGCATGAGCAGTACATGCTTGATGTCTTCTCTTCTCCTAGGGCTCATGCT	1588
Qy	1558	GGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGC	1617
Db	1589	GGGTACTTTGTGGCTTAGTGTAAGGTTCTTGTGCTGTAACCAGGTATCTGAGTATAGC	1648
Qy	1618	CAGAAAGGTGAAGGAGACATAAGGC	1642
Db	1649	AACGAAGGTCAAGGAGGCATAATGC	1673

RESULT 3

AY404344

LOCUS AY404344 1180 bp DNA linear GSS 12-DEC-2003

DEFINITION Pan troglodytes HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY404344

VERSION AY404344.1 GI:39760321

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 1180)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1180)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers
source 1. .1180
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene <1. .>1180
/locus_tag="HCM1859"

ORIGIN

Query Match 37.0%; Score 857.4; DB 29; Length 1180;
Best Local Similarity 73.0%; Pred. No. 1.3e-232;
Matches 861; Conservative 0; Mismatches 319; Indels 0; Gaps 0;

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Qy      460 GGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCC 519
      |||||||
Db       1  GGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCC 60

Qy      520 TTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCG 579
      |||||||
Db      61  TTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCG 120

Qy      580 CTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCT 639
      |||||||
Db     121  CTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCT 180

Qy      640 GACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTG 699
      |||||||
Db     181  GACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTG 240

Qy      700 CAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGA 759
      |||||||
Db     241  CAGGAGGCAATGGGACATGCAGTCTACATTTGACAACACCATCAAGGAGCATTTCCAGA 300

Qy      760 AGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAC 819
      |||||||
Db     301  AGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTNNNTTAAC 360

Qy      820 TGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCT 879
      ||
Db     361  TGNNNTTGCCTTTGATTTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 420

Qy      880 GATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGG 939
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Db     421  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 480

Qy      940 GGACTCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGA 999
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Db     481  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 540

Qy     1000 AATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTG 1059
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Db     541  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 600

Qy     1060 TCAGTGTTCTCATTTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTG 1119
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Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13284 row: 1 column: 23
 High quality sequence start: 17
 High quality sequence stop: 671.

FEATURES
 source Location/Qualifiers
 1. .879
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6043558"
 /tissue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_92"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 36.8%; Score 853.2; DB 13; Length 879;
 Best Local Similarity 99.0%; Pred. No. 1.8e-231;
 Matches 869; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy	780	CTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTA	ACTCTGACTTTGCCTTTGATTTTG	839
Db	1	CTCATCTTCTACTGAAAGCAGAGATGTGGTTCATTA	ACTCTGACTTTGCCTTTGATTTTG	60
Qy	840	CTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAAC		899
Db	61	CTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAAC		120
Qy	900	CAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTG		959
Db	121	CAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTG		180
Qy	960	TGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACA		1019
Db	181	TGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACA		240
Qy	1020	ATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCA		1079
Db	241	ATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCA		300
Qy	1080	AAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCC		1139
Db	301	AAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCC		360
Qy	1140	TGGCTCACCCAAGCATCCGTCTGTTTGTGACCCACGGCGGGCAGAATAGCATAATGGAGG		1199
Db	361	TGGCTCACCCAAGCATCCGTCTGTTTGTGACCCACGGCGGGCAGAATAGCATAATGGAGG		420

Qy 1200 CCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACA 1259
 |||
 Db 421 CCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACA 480
 Qy 1260 TGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAG 1319
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 Db 481 TGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAG 540
 Qy 1320 AGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAG 1379
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 Db 541 AGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAG 600
 Qy 1380 TGGCTGCCAGTGTCTATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCT 1439
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 Db 601 TGGCTGCCAGTGTCTATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCT 660
 Qy 1440 GGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGC 1499
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 Db 661 GGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGC 720
 Qy 1500 AGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGG 1559
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 Db 721 AGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGG 780
 Qy 1560 GGACTCTATGGCTTTGT-GGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCC 1618
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 Db 781 GGACTCTATGGCTTTGTGGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCTTGGGGCC 840
 Qy 1619 AGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTG 1656
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 Db 841 ACAAAGGGAAGGAGACCTAAAGCCAGGTGCACCCTTG 878

RESULT 5

CD050395

LOCUS CD050395 916 bp mRNA linear EST 09-MAY-2003

DEFINITION AGENCOURT_13977999 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CD050395

VERSION CD050395.1 GI:30487290

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 916)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jamie Thompson, University of WI

cDNA Library Preparation: Gina Zastrow-Hayes

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: NDKM37 row: m column: 04
High quality sequence start: 12
High quality sequence stop: 721.

FEATURES
source Location/Qualifiers
1. .916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic trophoblasts, made from WA01 stem cells"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_173"
/note="Vector: pDONR201; Site_1: attP2; Site_2: attP1;
LIBR_PRIMING - oligo dT; METHOD - full-length enriched;
LIBR_PROVIDER - Bradfield"

ORIGIN

Query Match 31.8%; Score 738; DB 14; Length 916;
Best Local Similarity 95.0%; Pred. No. 1.4e-198;
Matches 795; Conservative 0; Mismatches 36; Indels 6; Gaps 3;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	54	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	113
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	114	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	173
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	174	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	233
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	234	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	293
Qy	241	CAAAAGAGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	294	CAAAAGAGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	353
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	354	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	413
Qy	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	414	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	473
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	474	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	533
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	534	CTTCGACAT-GTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	592

Qy 541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600
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 Db 593 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 652
 Qy 601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG 660
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 Db 653 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG 712
 Qy 661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
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 Db 713 GGGCCGAGTGAAGAATTTTCTGATNGTCTTTAGTTTCTGCAGGAAGCAACAGCACATGCA 772
 Qy 721 GTCTACATTTGACAACACCATCAAGGAACA--TTTCACAGAAGGCTCTAGGCCAGTTTTG 778
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 Db 773 GTCTACATTTGACAACACCATCCAAGGACATTTTTCACAGAGGGCTCTAGGGCCAGTTTT 832
 Qy 779 TCTC---ATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTT 832
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 Db 833 GTCCTCAATCTTCTACTGAAAAGCAAAAGTTGGTGGGTTCATTTAACCTCTGGACTT 889

RESULT 6

AY404345

LOCUS AY404345 1185 bp DNA linear GSS 12-DEC-2003

DEFINITION Mus musculus HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY404345

VERSION AY404345.1 GI:39760322

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1185)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1185)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .1185

/organism="Mus musculus"

/mol_type="genomic DNA"

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gene      /db_xref="taxon:10090"
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ORIGIN
Query Match      31.6%; Score 733.8; DB 29; Length 1185;
Best Local Similarity 76.8%; Pred. No. 2.4e-197;
Matches 910; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

Qy      458 ATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGT 517
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Db      1   ATGGACTTCTTAAAAAATGAGAACTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGT 60

Qy      518 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTC 577
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Db      61 TCTTTGCTAATTGTTGAAAAGCTTGGGAAACGATTTGTGTCCTTTCTCCCTTTCAATTT 120

Qy      578 GGCTCTTTGGAATTTGGGCTACCAA---TCCCCTTGTCTTATGTTCCAGTATCCGTTCC 634
        ||| | |||| | ||||| ||||| | ||||| ||||| | |||||
Db      121 AGCTATATGGACTTTGGGTTACCAAGCGCCCCCTTGTCTATGCTCCAGTGTATGGTTCT 180

Qy      635 TTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGT 694
        || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||| |
Db      181 GGTCTAACTGACCAAATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTCTGAT 240

Qy      695 TTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTTC 754
        |||| | || |||| | | || | ||| | |||| | || |||| | |||||
Db      241 TTCTCCATGAAGCAAAGGGAAATCCTTTCTCAGTATGACAGCACTATCCAGGAGCATTTT 300

Qy      755 ACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTTCATT 814
        ||||| ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |
Db      301 GTGGAAGGCTCTCAGCCAGTGTGTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCT 360

Qy      815 AACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGA 874
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Db      361 AACTCTGACTTTGCTTTGGATTTTGCTCGTCCCTGTTTCCCAACACAGTCTATGTGGGA 420

Qy      875 GGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAG 934
        || || |||| | ||||| || | ||| ||||| ||||| ||||| || || |||
Db      421 GGTTTACTGGACAAACCTGTTTCAGCCAATACCCCAAGACTTGGAGAATTTTATCTCTCAG 480

Qy      935 TTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAAT 994
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Db      481 TTTGGAGACTCAGGTTTTGTCTTGTGGCCCTGGGCTCTATAGTGAGCATGATTCAGTCC 540

Qy      995 CCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG 1054
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Db      541 AAGGAAATTATTAAGGAGATGAACAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGG 600

Qy      1055 AAGTGTCAAGTGTCTCATTGGCCCCAAAGATGTCCACCTGGCTGCAAAATGTGAAAATTTGTG 1114
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Db      601 ACATGTAAGACTTCTCATTGGCCCCAAAGATGTGAGTTTGGCCCCAAATGTCAAAATCATG 660

Qy      1115 GACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCAC 1174
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Db      661 GATTGGCTTCACAGACTGACCTTCTAGCTCACCTAGCATTCGTCTGTTTGTCACTCAT 720

```

Qy 1175 GCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCT 1234
 || ||| ||| || | ||||| ||| ||||| || ||||| ||| ||
 Db 721 GGAGGGATGAACAGTGTGATGGAGGCTGTCCATCATGGAGTACCCATGGTGGGGATTCCA 780
 Qy 1235 CTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCT 1294
 | ||| ||||| ||||| ||||| ||||| ||||| || || ||||| |||||
 Db 781 TTTTTTTTTGACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTCT 840
 Qy 1295 ATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAA 1354
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 Db 841 ATTCAGCTACAGACGCTCAAGGCAGAGTCATTTGCGCTCACCATGAAAAAATCATAGAA 900
 Qy 1355 GACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTC 1414
 ||||| ||||| || ||| |||| ||| | ||| || ||||| |||
 Db 901 GACAAGAGGTACAAGTCTGCAGCAATGGCCTCCAAGATTATCAGGCACTCCCACCCACTG 960
 Qy 1415 AGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACG 1474
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 Db 961 ACCCCTGCCAGAGGCTTTTGGGCTGGATAGATCATATCTTGACAGACAGGGGGTGCAGCA 1020
 Qy 1475 CACCTCAAGCCCTATGTCTTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTT 1534
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 Db 1021 CATCTCAAGCCATATGCTTTCCAGCAGCCATGGCATGAGCAGTACATGCTTGATGTCTTC 1080
 Qy 1535 GTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATG 1594
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 Db 1081 CTCTTTCTCCTAGGGCTCATGCTGGGTACTTTGTGGCTTAGTGTAAGGTTCTTGTTGCT 1140
 Qy 1595 GCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAA 1639
 | | ||| ||| || || | |||| ||||| |||||
 Db 1141 GTAACCAGGTATCTGAGTATAGCAACGAAGGTCAAGGAGGCATAA 1185

RESULT 7

AK041045

LOCUS AK041045 1353 bp mRNA linear HTC 19-SEP-2003

DEFINITION Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530069C13 product:hypothetical UDP-glucuronosyl and UDP-glucosyl transferase containing protein, full insert sequence.

ACCESSION AK041045

VERSION AK041045.1 GI:26334156

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1353)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

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FEATURES                      Location/Qualifiers
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                              /db_xref="MGI:2405959"
                              /db_xref="taxon:10090"
                              /clone="A530069C13"
                              /sex="male"
                              /tissue_type="aorta and vein"
                              /clone_lib="RIKEN full-length enriched mouse cDNA library"
                              /dev_stage="adult"
    CDS                       83. .991
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                              protein (InterPro|IPR002213, evidence: InterPro)
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                              /codon_start=1
                              /protein_id="BAC30796.1"
                              /db_xref="GI:26334157"
                              /translation="MAAHRRWLLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQ
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                              FVSFLPFQFSYMDFGLPSAPLSYAPVYGSGLTDQMDFWGRVKNFLMFLDFSMKQREIL
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ORIGIN

Query Match 31.5%; Score 731.6; DB 11; Length 1353;
 Best Local Similarity 73.1%; Pred. No. 1.1e-196;
 Matches 981; Conservative 0; Mismatches 354; Indels 7; Gaps 3;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db      16 AGGGTCCCTTAGTGGGGCACAGCTCTTTAGGTGTGCAACCTGTGTGTCAGGGCTCCACATAT 75

Qy      61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCCT 120
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Db      76 TCTACAGATGGCAGCACATCGGCGTTGGCTTCTCATGAGCTTCCTTTTCTTGAGGTTAT 135

Qy     121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Db     136 TCTCTTGGAGGCTGCAAAAATCCTGACTATATCTACACTGAGTGCAAGCCATTATATAGT 195

Qy     181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
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Db     196 GATAAGCCGTGTGTCGCAAGTTCCTCATGAAGGTGGCCACAATGTGACCAAACTTCTTTA 255

Qy     241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
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Db     256 TGAAA---GTGCTAATATCCAGATTTTAGAAAGGAAAAACCATCATATCAAGTTATTAA 312

Qy     301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA 360
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Db     313 TTGGCGTCCACCTGAAGATCAGGAAAAGAAATTTGCTGATCTTAGGCATCGACTTACAGA 372

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Qy 361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
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Qy 421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA 480
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 Db 433 GGACTTATGCAGTCAATTATTAAGCAGAAAGGACATCATGGACTTCTTAAAAAATGAGAA 492

Qy 481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
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 Db 493 CTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGTTCTTTGCTAATTGTTGAAAAGCT 552

Qy 541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
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 Db 553 TGGGAAACGATTTGTGTCCTTTCTTCCCTTTCAATTTAGCTATATGGACTTTGGGTTACC 612

Qy 601 AA---TCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTT 657
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 Db 613 AAGCGCCCCCTTGTCTATGCTCCAGTGTATGGTTCTGGTCTAACTGACCAAATGGACTT 672

Qy 658 CTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACAT 717
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Qy 718 GCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTT 777
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 Db 733 CCTTTCTCAGTATGACAGCACTATCCAGGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTT 792

Qy 778 GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTT 837
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 Db 793 GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGACTTTGCTTTGGATTT 852

Qy 838 TGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAA 897
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 Db 853 TGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGG-TTACTGGACAAACCTGTTCA 911

Qy 898 ACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCT 957
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 Db 912 GCCAATACCCAAGACTTGGAGAATTTTATCTCTCAGTTTGGAGACTCAGGTTTTGTCT 971

Qy 958 TGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAA 1017
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 Db 972 TGTGGCCCTGGGCTCTATAGTGAGCATGATTCAGTCCAAGGAAATTATTAAGGAGATGAA 1031

Qy 1018 CAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCC 1077
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 Db 1032 CAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAGACTTCTCATTGGCC 1091

Qy 1078 CAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCT 1137
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 Db 1092 CAAAGATGTCAGTTTGGCCCCAAATGTCAAATCATGGATTGGCTTCACAGACTGACCT 1151

Qy 1138 CCTGGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGA 1197
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 Db 1152 TCTAGCTCACCTAGCATTCGTCTGTTTGTCACTCATGGAGGGATGAACAGTGTGATGGA 1211

Qy 1198 GGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAA 1257

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Db      1212 GGCTGTCCATCATGGAGTACCCATGGTGGGGATTCCATTTTTTTTTTGACCAACCTGAAAA 1271

Qy      1258 CATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGC 1317
      ||||| ||||| ||||| || || ||||| ||||| || || ||||| |||||
Db      1272 CATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTCTATTTCAGCTACAGACGCTCAAGGC 1331

Qy      1318 AGAGACATTGGCTCTTAAGATG 1339
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Db      1332 AGAGTCATTTGCGCTCACCATG 1353

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RESULT 8

BI102968

LOCUS BI102968 978 bp mRNA linear EST 26-JUN-2001

DEFINITION 60288578F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5043978
5', mRNA sequence.

ACCESSION BI102968

VERSION BI102968.1 GI:14553861

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 978)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11120 row: k column: 19

High quality sequence stop: 812.

FEATURES

source

Location/Qualifiers

1. .978

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5043978"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_Kid14"

/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library. |"

ORIGIN

Query Match 22.5%; Score 522.4; DB 12; Length 978;

Best Local Similarity 77.7%; Pred. No. 4.7e-137;

Matches 682; Conservative 0; Mismatches 191; Indels 5; Gaps 4;

Qy	644	GATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGG	703
Db	1	GACCAAATGGACTTTTGGGGCCGAGTGAAGAACATTCTGATGTTCTTTTCATTTACCAAG	60
Qy	704	AGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGC	763
Db	61	AAGCGAAGGGACATCTTTTCTCAATATGGCAATACTGTCCAGGAGCATTTTGC GGAAGGC	120
Qy	764	TCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGAC	823
Db	121	TCTCAGCCAGTGTTGTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGAC	180
Qy	824	TTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATG	883
Db	181	TTTGCCTTGGATTTTGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTG	240
Qy	884	GAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGAC	943
Db	241	GACAAACCTGTTTCAGCCAATACCCCAAGACTTGGAGGATTTTATCTCTCAGTTTGGAGAC	300
Qy	944	TCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATC	1003
Db	301	TCAGGTTTTGTCTTGTGGCCCTGGACTCTGTAGTGAGCATGATTCAGTCCAAGGAAAT	360
Qy	1004	TTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAC	1063
Db	361	ATTAAGGAGATGAACAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAG	420
Qy	1064	TGTTCTCATTTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTT	1123
Db	421	AGTTCTCATTTGGCCCAAAGATGTCAGTTTGGCCCAAATGTCAAATCATGGATTGGCTT	480
Qy	1124	CCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAG	1183
Db	481	CCACAGATTGACCTTCTAGCTCACCTAGCATTCGTCTGTTTGTACCCATGGGGGGATG	540
Qy	1184	AATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGA	1243
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Qy	1244	GACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTGAGTTA	1303
Db	601	GACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTCTATTGAGCTA	660
Qy	1304	AAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGA	1363
Db	661	CAGACACTCAAGGCAGAGTCATTTTGGCTCACCATGAAAGAAGTCATAGAAGACCAGAGG	720
Qy	1364	TACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACA	1423
Db	721	TACAAGACTGCAGCA-TGGCCTCCAAGGTTATCAGGAACCTCCACC--AATGACCCTGGC	777
Qy	1424	CAGCGGCTGGTGGGCTGGATTGACCACGTC-CTCCAGACAGGGGGCGCGACGCACCTCAA	1482
Db	778	CAGAGGCTTGTGGGCTGGATTGATCACATCTTTGCAGACAGGGGGTGCAGCCCATCTCAA	837

Qy 1483 GCCCTATGTCTT-TCAGCAGCCCTGGCATGAGCAGTAC 1519
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 Db 838 AGCATATGGCTTCCCAGCAGGCTTGGCATAACGAGTAC 875

RESULT 9

BI559553

LOCUS BI559553 761 bp mRNA linear EST 05-SEP-2001

DEFINITION 603252894F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295502 5', mRNA sequence.

ACCESSION BI559553

VERSION BI559553.1 GI:15446867

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 761)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11747 row: k column: 23

High quality sequence stop: 726.

FEATURES

source

Location/Qualifiers

1. .761

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5295502"

/lab_host="DH10B"

/clone_lib="NIH_MGC_97"

/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTTVN-3', size-selected for average

insert size 2.2 kb and normalized to ROT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 21.1%; Score 488.6; DB 12; Length 761;

Best Local Similarity 80.7%; Pred. No. 1.9e-127;

Matches 608; Conservative 0; Mismatches 139; Indels 6; Gaps 3;

IMAGE:2663780 3' similar to SW:CGT_RAT Q09426
 2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR ;,
 mRNA sequence.

ACCESSION AW173071
 VERSION AW173071.1 GI:6439019
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 694)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40UP from Gibco
 High quality sequence stop: 412.

FEATURES Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2663780"
 /lab_host="DH10B"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NbHL19W, testis NHT, and B-cell
 NCI_CGAP_GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 20.0%; Score 463.6; DB 10; Length 694;
 Best Local Similarity 83.5%; Pred. No. 2.4e-120;
 Matches 537; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

QY	268	TAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGACCTGAAGATCATCAAAG	327
Db	643	TATAAAGAGAAGCAAAATTCATACAGGTATCCGGGTGGTTTTTCACCTAAGATCATCAAAA	584
QY	328	AGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGGTGGCAGAGGAAAAATT	387
Db	583	AGAA-TTAAGAAGCATTTTGATAGCTACATAGAAACAGCATTGGATGGCAGAAAAGAATC	525
QY	388	TGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCATTTTTTAAATAG	447

[illegible]

Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: FQY8035 row: J column: 24
 Seq primer: TAGAAGGCACAGTCGAGG.

FEATURES Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 6BOV"
 /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
 Library made with RNA pooled from multiple tissues
 including liver, lung, hypothalamus, pituitary, and
 placenta/endometrium."

ORIGIN

Query Match 19.7%; Score 457.6; DB 14; Length 659;
 Best Local Similarity 81.1%; Pred. No. 1.2e-118;
 Matches 532; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

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Db	658	AGAAAGGATGTCATGAAGTCTTTAAAGAATGAGAACTTCGACCTGGTGATAGTGGAATG	599
Qy	506	TTTGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTT	565
Db	598	TTTGACTACTGTCCTTTCTTGGTTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTC	539
Qy	566	TCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTA	625
Db	538	CCTTCCGCACCTGGGCACCGTGGACTTTGGGCTACCAAGCCCTCTGTCTTATGTGCCAGTG	479
Qy	626	TTCCGTTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATG	685
Db	478	TTCTACTCCTTGTTAACGGACCAGATGGACTTCTGGGGCCGAGTAAAGAACTTCCTGATG	419
Qy	686	TTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAG	745
Db	418	TTCTTTGAGTTCTTCAAGAAGCAGTGGAATCCAGTCTGCATATGATGACACCATCAAG	359
Qy	746	GAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTG	805
Db	358	GAGCATTTCCCGGACGACTCTAGGCCAGTTTGTCTCATCTTCTAACAAAAGCAGAGCTG	299
Qy	806	TGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTT	865
Db	298	TGGTTTGTTAACACCGACTTTGCCTTTGATTTTGCTCAGCCCTGCTTCCCAACACTGTG	239
Qy	866	TATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAATTTC	925
Db	238	TGTATTGGAGGTTTAAATGTCAAACCTGTAAACCAGTACCACAAGAATTTGAGAATTTTC	179
Qy	926	ATTGCCAAGTTTGGGGACTCTGGTFTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACC	985

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1723)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .1723
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM_DB:D630011D02"
 /db_xref="MGI:2422342"
 /db_xref="taxon:10090"
 /clone="D630011D02"
 /tissue_type="kidney"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="0 day neonate"

misc_feature 1. .1723
 /note="hypothetical UDP-glucuronosyl and UDP-glucosyl transferase containing protein (InterPro|IPR002213, evidence: InterPro)"

ORIGIN

Query Match 19.5%; Score 452.6; DB 11; Length 1723;
 Best Local Similarity 69.1%; Pred. No. 4.9e-117;
 Matches 649; Conservative 0; Mismatches 284; Indels 6; Gaps 2;

Qy		1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA	60
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Qy		61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db		101	TCTACAGATGGCAGCACATCGGCGTTGGCTTCTCATGAGCTTCCTTTTCTTGAGGTTAT	160
Qy		121	GCTCTCAGAGGCTGCCAAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db		161	TCTCTTGGAGGCTGCAAAAAATCCTGACTATATCTACACTGAGTGCAAGCCATTATATAGT	220
Qy		181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db		221	GATAAGCCGTGTGTCGCAAGTTCTTCATGAAGGTGGCCACAATGTGACCAAACTTCTTTA	280
Qy		241	CAAAAGAGGTCTTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db		281	TGAAA---GTGCTAATATCCCAGATTTTAGAAAGGAAAACCATCATATCAAGTTATTAA	337
Qy		301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Db		338	TTGGCGTCCACCTGAAGATCAGGAAAAGAAATTTGCTGATCTTAGGCATCGACTTACAGA	397
Qy		361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db		398	AGAAATAACTTATGGCAGGTCCAACATCACACCCTTCTAAAGATCCATCAATACTTTGG	457
Qy		421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db		458	GGACTTATGCAGTCAATTATTAAGCAGAAAGGACATCATGGACTTCTTAAAAAATGAGAA	517
Qy		481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAAGCT	540
Db		518	CTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGTTCTTTGCTAATTGTTGAAAAGCT	577
Qy		541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db		578	TGGGAAACGATTTGTGTCCTTCTTCCCTTCAATTTAGCTATATGGACTTTGGGTTACC	637
Qy		601	AA---TCCCCCTTGCTTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTT	657
Db		638	AAGCGCCCCCTTGTCCTATGCTCCAGTGTATGGTTCCTGGTCTAACTGACCAAATGGACTT	697
Qy		658	CTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACAT	717
Db		698	CTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTGATTCTCCATGAAGCAAAGGGAAAT	757
Qy		718	GCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTT	777
Db		758	CCTTTCTCAGTATGACAGCACTATCCAGGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTT	817
Qy		778	GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTA ACTCTGACTTTGCCTTTGATTT	837
Db		818	GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTGTCAACTCTGACTTTGCTTTGGATTT	877
Qy		838	TGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAA	897

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Db      878 TGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTGGACAAACCTGTTCA 937

Qy      898 ACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTT 936
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Db      938 GCCAATACCCCAAGTAAGTGACAAATTAGCTCTCACTTT 976

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RESULT 13

CB952493

LOCUS CB952493 724 bp mRNA linear EST 29-APR-2003

DEFINITION AGENCOURT_13692869 NIH_MGC_176 Mus musculus cDNA clone
IMAGE:30303573 5', mRNA sequence.

ACCESSION CB952493

VERSION CB952493.1 GI:30208612

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 724)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Michael Brownstein Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDCM74 row: e column: 22

High quality sequence stop: 541.

FEATURES

source

Location/Qualifiers

1. .724

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:30303573"

/lab_host="DH10B (T1-phage-resistant)"

/clone_lib="NIH_MGC_176"

/note="Organ: kidney; Vector: pDNR-LIB; Site_1: SfiI
(ggcattatggcc); Site_2: SfiI (ggccgcctcggcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:

5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and

5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech

Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.

Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 19.4%; Score 450; DB 14; Length 724;
Best Local Similarity 78.3%; Pred. No. 1.9e-116;

LOCUS CB158774 481 bp mRNA linear EST 29-JAN-2003
 DEFINITION K-EST0218183 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-14-D07
 5', mRNA sequence.
 ACCESSION CB158774
 VERSION CB158774.1 GI:28143912
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 481)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 14 row: D column: 07
 High quality sequence stop: 481.
 FEATURES Location/Qualifiers
 source 1. .481
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L18POOL1n1-14-D07"
 /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
 /lab_host="Top10F"
 /clone_lib="L18POOL1n1"
 /note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
 Site_2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 6(9): 791-806. RNA was prepared from harvested cell
 culture."

ORIGIN

Query Match 19.2%; Score 444.4; DB 14; Length 481;
 Best Local Similarity 99.8%; Pred. No. 6.3e-115;
 Matches 445; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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 Db 36 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 95
 Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 96 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 155
 Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 156 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGATGCCATTATCTACT 215

Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	216	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	275
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	276	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	335
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Db	336	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	395
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	396	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	455
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATA	446
Db	456	GTTGCAGTGCAGTCATTTTTTAAATA	481

RESULT 15

AI694348/c

LOCUS AI694348 583 bp mRNA linear EST 17-DEC-1999

DEFINITION wd45g04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2331126 3' similar to SW:CGT_MOUSE Q64676
2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR ; ,
mRNA sequence.

ACCESSION AI694348

VERSION AI694348.1 GI:4971688

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 583)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 929 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 462.

FEATURES Location/Qualifiers

source 1. .583

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2331126"

/lab_host="DH10B"

/clone_lib="Soares_NFL_T_GBC_S1"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

Query Match 19.1%; Score 442; DB 9; Length 583;
Best Local Similarity 85.0%; Pred. No. 3.3e-114;
Matches 493; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Search completed: May 16, 2004, 14:01:53
Job time : 8801 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 04:18:54 ; Search time 14319 Seconds
(without alignments)
7022.546 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 aggggtcccttagccggg'gcgc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
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25: em_pl:*
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27: em_sts:*

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28: em_un:*
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35: em_htg_rod:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			Query				ID	Description
	No.	Score	Match	Length	DB			
	1	2320	100.0	2320	6	AX697213	AX697213	Sequence
	2	2320	100.0	2320	9	AY358416	AY358416	Homo sapi
	3	2310.2	99.6	2341	6	AX136141	AX136141	Sequence
	4	2310.2	99.6	2341	6	BD123523	BD123523	Secretory
	5	2310.2	99.6	2341	9	AK075383	AK075383	Homo sapi
	6	2102.8	90.6	2944	6	AX548037	AX548037	Sequence
	7	1281.6	55.2	2082	6	AX359921	AX359921	Sequence
	8	1281.6	55.2	2797	6	AX155211	AX155211	Sequence
	9	1281.6	55.2	2823	6	AX714604	AX714604	Sequence
	10	1281.6	55.2	2823	9	AK057066	AK057066	Homo sapi
	11	1280	55.2	2086	6	AX327327	AX327327	Sequence
	12	1212	52.2	1572	6	AX359923	AX359923	Sequence
c	13	957.6	41.3	88948	2	AC008947	AC008947	Homo sapi
	14	957.6	41.3	179513	9	AC016612	AC016612	Homo sapi
	15	944.8	40.7	1569	6	AX155213	AX155213	Sequence
	16	912.4	39.3	2210	10	AK128903	AK128903	Mus muscu
	17	912.2	39.3	2192	10	BC034837	BC034837	Mus muscu
	18	912.2	39.3	2196	10	BC022134	BC022134	Mus muscu
	19	910.8	39.3	2212	6	AX155214	AX155214	Sequence
	20	909.2	39.2	2228	10	BC025940	BC025940	Mus muscu
	21	789	34.0	1569	6	AX155216	AX155216	Sequence
	22	595.4	25.7	148069	2	AC025476	AC025476	Homo sapi
	23	595.2	25.7	770	6	AX136483	AX136483	Sequence
	24	595.2	25.7	770	6	BD123723	BD123723	Secretory
	25	593.4	25.6	1842	6	AX747286	AX747286	Sequence
	26	593.4	25.6	1842	9	AK091977	AK091977	Homo sapi
	27	592.2	25.5	102255	2	AC026735	AC026735	Homo sapi
	28	575.4	24.8	5002	9	AK125803	AK125803	Homo sapi
	29	573.6	24.7	125145	2	AC022136	AC022136	Homo sapi
	30	573.4	24.7	3108	9	BC035012	BC035012	Homo sapi
c	31	538.8	23.2	148069	2	AC025476	AC025476	Homo sapi
c	32	538.4	23.2	594	6	AX136632	AX136632	Sequence
c	33	538.4	23.2	594	6	BD123872	BD123872	Secretory

34	444.8	19.2	88948	2	AC008947	AC008947 Homo sapi
35	433.6	18.7	105885	9	AC008860	AC008860 Homo sapi
c 36	320.6	13.8	156499	2	AC132893	AC132893 Mus muscu
37	308.2	13.3	251769	2	AC117913	AC117913 Rattus no
38	308	13.3	156499	2	AC132893	AC132893 Mus muscu
c 39	245.2	10.6	211178	10	AC139209	AC139209 Mus muscu
c 40	239.2	10.3	125145	2	AC022136	AC022136 Homo sapi
c 41	239.2	10.3	165304	9	AC112204	AC112204 Homo sapi
42	174	7.5	1879	5	AF129809	AF129809 Gallus ga
43	167.2	7.2	3598	10	AK128994	AK128994 Mus muscu
44	167.2	7.2	4185	10	RNU07683	U07683 Rattus norv
45	165.6	7.1	2633	10	RATCERUDPG	L21698 Rat ceramid

ALIGNMENTS

RESULT 1

AX697213

LOCUS AX697213 2320 bp DNA linear PAT 02-APR-2003

DEFINITION Sequence 281 from Patent WO0078961.

ACCESSION AX697213

VERSION AX697213.1 GI:29498151

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0078961-A 281 28-DEC-2000;
Genentech Inc. (US)

FEATURES Location/Qualifiers

source 1. .2320
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2320; DB 6; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180

Db	121		GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181		GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181		GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241		CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241		CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301		TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Db	301		TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Qy	361		AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361		AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421		GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421		GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481		CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481		CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601		AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601		AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020

Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
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Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
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Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTGAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTGAGTTAAAGAAGCTCAAGGCAGA	1320
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Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTGAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTGAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860

Qy 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
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 Db 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920

Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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 Db 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC 1980

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 Db 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040

Qy 2041 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT 2100
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 Db 2041 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT 2100

Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160

Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220

Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA 2280
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 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA 2280

Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 2

AY358416

LOCUS AY358416 2320 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA71169 glucuronosyltransferase (UNQ842) mRNA, complete cds.

ACCESSION AY358416

VERSION AY358416.1 GI:37181956

KEYWORDS FLI_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2320)

AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale

Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment

JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 2320)
AUTHORS Clark, H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES
source 1. .2320
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/mol_type="mRNA"
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gene 1. .2320
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ORIGIN

Query Match 100.0%; Score 2320; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCT	120
QY	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
QY	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
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Db	241		CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301		TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Db	301		TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Qy	361		AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
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Db	601		AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661		GGGCCGAGTGAAGAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
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Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
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Db	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
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Db	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
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Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
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Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
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Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
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Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
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Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980

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RESULT 3

AX136141

LOCUS AX136141 2341 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 63 from Patent EP1067182.

ACCESSION AX136141

VERSION AX136141.1 GI:14272549

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
 Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: EP 1067182-A 63 10-JAN-2001;
 Helix Research Institute (JP)

FEATURES Location/Qualifiers

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Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	687	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	746
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
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Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	807	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	866
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	867	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	926
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
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Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
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Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560

BD123523
 LOCUS BD123523 2341 bp DNA linear PAT 18-SEP-2002
 DEFINITION Secretory protein or membrane protein.
 ACCESSION BD123523
 VERSION BD123523.1 GI:23218468
 KEYWORDS JP 2002017376-A/32.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2341)
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
 Hayashi,K.
 TITLE Secretory protein or membrane protein
 JOURNAL Patent: JP 2002017376-A 32 22-JAN-2002;
 HELIX RESEARCH INSTITUTE
 COMMENT OS Homo sapiens (human)
 PN JP 2002017376-A/32
 PD 22-JAN-2002
 PF 07-JUL-2000 JP 2000253173
 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
 PI SUGIYAMA,
 PI KOJI HAYASHI
 PC
 C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ 10,
 PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC
 Secretory protein or membrane protein
 FH Key Location/Qualifiers
 FT CDS (94)..(1662).
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 source 1..2341
 /organism="Homo sapiens"
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Query Match 99.6%; Score 2310.2; DB 6; Length 2341;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
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QY	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	87	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	146
QY	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	147	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	206
QY	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	207	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	266

Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
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Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
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Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
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Db	927	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	986
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	987	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1046
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAA	1080
Db	1047	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAA	1106
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Db	1227	 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1286
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
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Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
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Db	1407	 GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1466
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Db	1527	 GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1586
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1587	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1646
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RESULT 5

AK075383

LOCUS AK075383 2341 bp mRNA linear PRI 03-SEP-2002
 DEFINITION Homo sapiens cDNA PSEC0073 fis, clone NT2RP2002934, weakly similar
 to UDP-GLUCURONOSYLTRANSFERASE 2C1 MICROSOMAL (EC 2.4.1.17).

ACCESSION AK075383

VERSION AK075383.1 GI:22761433

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,
 Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
 Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.

TITLE HRI human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2341)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
 sequencing, clone selection and full insert sequencing; Helix
 Research Institute (supported by Japan Key Technology Center etc.);
 cDNA library construction: Institute of Medical Science, University
 of Tokyo, Laboratory of Genome Structure, Human Genome Center.

FEATURES Location/Qualifiers

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Query Match      99.6%; Score 2310.2; DB 9; Length 2341;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACC	600
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Qy	601		AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTG	660
Db	627		AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTG	686
Qy	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	687		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	746
Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
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Db	807		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC	866
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Qy	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
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Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
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Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1647	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1706
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Db	1767	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1826
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1827	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1886
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AX548037

LOCUS AX548037 2944 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 13 from Patent WO02066654.

ACCESSION AX548037

VERSION AX548037.1 GI:25813133

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Astromoff,A., Au-Young,J., Baughn,M.R., Ding,L., Duggan,B.M.,
 Forsythe,I.J., Gietzen,K.J., Griffin,J.A., Lee,E.A., Lu,Y.,
 Richardson,T.W., Ring,H.Z., Sanjanwala,M.M., Swarnakar,A.,
 Walia,N.K., Warren,B.A., Xu,Y., Yue,H. and Zebarjadian,Y.

TITLE Drug metabolizing enzymes

JOURNAL Patent: WO 02066654-A 13 29-AUG-2002;

Incyte Genomics, Inc. (US)

FEATURES

Location/Qualifiers

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/note="Incyte ID No: 7486594CB1"

ORIGIN

Query Match 90.6%; Score 2102.8; DB 6; Length 2944;

Best Local Similarity 95.5%; Pred. No. 0;

Matches 2216; Conservative 0; Mismatches 2; Indels 102; Gaps 1;

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Qy 301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
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Qy 361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
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 Db 462 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 521

Qy 421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
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Qy 481 CTTGCAGATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
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 Db 582 CTTGCAGATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 641

Qy 541 TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
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 Db 642 TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 701

Qy 601 AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660
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Db	1062	 GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1121
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1122	 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1181
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1182	 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1241
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1242	 GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1301
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1302	 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1361
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTGAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1362	 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTGAGTTAAAGAAGCTCAAGGCAGA	1421
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1422	 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1481
Qy	1381	GGCTGCCAGTGTGTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1482	 GGCTGCCAGTGTGTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1541
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1542	 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1601
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1602	 GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1661
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
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Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
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Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
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Qy	1861	CTTGTCTCTCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1962	CTTGTCTCTCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	2021
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	2022	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	2081
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	2082	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2141
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2142	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2201
Qy	2101	TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2202	TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2261
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2262	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2321
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2322	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2381
Qy	2281	AATAAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
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ORIGIN

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Query Match          55.2%;  Score 1281.6;  DB 6;  Length 2082;
Best Local Similarity 85.9%;  Pred. No. 0;
Matches 1422;  Conservative 0;  Mismatches 234;  Indels 0;  Gaps 0;

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Qy      7 CCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAGTGAG 66
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Db      84 CCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCTGCTTCTGTGGAAGTGAG 143

Qy      67 CATGGCTGGGCAGCGAGTGCTTCTTAGTGGGCTTCCTTCTCCCTGGGGTCTGCTCTC 126
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Db     144 CATGGTTGGGCAGCGGGTGCTGCTTCTTAGTGGCCTTCCTTCTTTCTGGGGTCTGCTCTC 203

Qy     127 AGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA 186
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Db     204 AGAGGCTGCCAAAATCCTGACAATATCTACACTGGGTGGAAGCCATTACCTACTGTTGGA 263

Qy     187 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAG 246
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Db     264 CCGGGTGTCTCAGATTCTTCAAGAGCATGGTCATAATGTGACTATGCTTCATCAGAGTGG 323

Qy     247 AGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCT 306
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Db     324 AAAGTTTTTGATCCCAGATATTAAAGAGGAGGAAAAATCATACCAAGTTATCAGGTGGTT 383

Qy     307 TGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGAAGAAAC 366
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Qy     367 TTTAGGTGGCAGAGGAAAAATTTGAAAACCTTATTAAATGTTCTAGAATACTTGGCGTTGCA 426
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Db     444 ATTGGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAAATATTTGGGACTCA 503

Qy     427 GTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGA 486
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Db     504 ATGTAGTTATTTGCTAAGCAGAAAGGATATAATGGATTCCTTAAAGAATGAGAACTATGA 563

Qy     487 CATGGTGATAGTTGAAACCTTTTGACTACTGTCCCTTTCCTGATTGCTGAGAAGCTTGGGAA 546
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Db     564 TCTGGTATTTGTTGAAGCATTTGATTCTGTCTTTCCTGATTGCTGAGAAGCTTGTGAA 623

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Qy	547	GCCATTTGTGGCCATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACCAATCCC	606
Db	624	ACCATTTGTGGCCATTCTTTCCACCACATTCCGGCTCTTTGGATTTTGGGCTACCAAGCCC	683
Qy	607	CTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCG	666
Db	684	CTTGTCTTATGTTCCAGTATTCCCTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCG	743
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Db	744	AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTCCAGGAGCCAATGGGACATGCAGTCTAC	803
Qy	727	ATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCT	786
Db	804	ATTTGACAACACCATCAAGGAGCATTTCCAGAAGGCTCTAGGCCAGTTTTGTCTCATCT	863
Qy	787	TCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACC	846
Db	864	TCTACTGAAAGCAGAGTTGTGGTTTGTAACTCTGATTTTGCTTTGATTTTGCCCGGCC	923
Qy	847	TCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAACCAGTACC	906
Db	924	CCTGCTTCCCAACACTGTTTATATTGGAGGCTTGATGGAAAACCTATTAACCAGTACC	983
Qy	907	ACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGTGACCTT	966
Db	984	ACAAGACTTGGACAACCTTCATTGCCAACTTTGGGGATGCAGGGTTTGTCTTGTGGCCTT	1043
Qy	967	GGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTT	1026
Db	1044	TGGCTCCATGTTGAACACCCATCAGTCCCAGGAAGTCTCAAGAAGATGCACAATGCCTT	1103
Qy	1027	TGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAAGATGT	1086
Db	1104	TGCCCACCTCCCTCAAGGAGTGATATGGACATGTGAGAGTTCTCATTGGCCCAAGATGT	1163
Qy	1087	CCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCA	1146
Db	1164	TCATTTGGCCACAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCA	1223
Qy	1147	CCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCA	1206
Db	1224	CCCCAGCATCCGTCTTTTGTCACTCATGGTGGGCAGAACAGCGTAATGGAGGCCATCCG	1283
Qy	1207	GCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCG	1266
Db	1284	TCATGGTGTGCCCATGGTGGGATTACCACTCAATGGAGACCAGCATGAAAACATGGTCCG	1343
Qy	1267	AGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATT	1326
Db	1344	AGTAGTAGCCAAAAATTATGGTGTCTCTATCCGGTTGAATCAGGTCACAGCCGACACACT	1403
Qy	1327	GGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGC	1386
Db	1404	GACACTTACAATGAAACAAGTCATAGAAGACAAGAGGTACAAGTCGGCAGTGGTGGCAGC	1463
Qy	1387	CAGTGTCTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGCTGGTGGGCTGGATTGA	1446

Query Match		55.2%;	Score 1281.6;	DB 6;	Length 2797;
Best Local Similarity		85.9%;	Pred. No. 0;		
Matches 1422;		Conservative	0;	Mismatches 234;	Indels 0; Gaps 0;
Qy	7	CCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAGTGAG	66		
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Qy	67	CATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTTGCTCTC	126		
Db	118	CATGGTTGGGCAGCGGGTGCTGCTTCTAGTGGCCTTCCTTCTTTCTGGGGTCTTGCTCTC	177		
Qy	127	AGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA	186		
Db	178	AGAGGCTGCCAAAATCCTGACAATATCTACACTGGGTGGAAGCCATTACCTACTGTTGGA	237		
Qy	187	CCGGGTTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAG	246		
Db	238	CCGGGTGTCTCAGATTCTTCAAGAGCATGGTCATAATGTGACTATGCTTCATCAGAGTGG	297		
Qy	247	AGGTCCTTTTATGCCAGATTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCT	306		
Db	298	AAAGTTTTTGATCCCAGATATTAAAGAGGAGGAAAAATCATACCAAGTTATCAGGTGGTT	357		
Qy	307	TGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAAC	366		
Db	358	TTCACCTGAAGATCATCAAAAAAGAATTAAGAAGCATTTTGATAGCTACATAGAAACAGC	417		
Qy	367	TTTAGGTGGCAGAGGAAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCA	426		
Db	418	ATTGGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAAATATTTGGGACTCA	477		
Qy	427	GTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAACTTCGA	486		
Db	478	ATGTAGTTATTTGCTAAGCAGAAAGGATATAATGGATTCCCTTAAAGAATGAGAACTATGA	537		
Qy	487	CATGGTGATAGTTGAAACTTTTGACTACTGTCTTTTCTGATTGCTGAGAAGCTTGGGAA	546		
Db	538	TCTGGTATTTGTTGAAGCATTTGATTTCTGTTCTTTTCTGATTGCTGAGAAGCTTGTGAA	597		
Qy	547	GCCATTTGTGGCCATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACCAATCCC	606		
Db	598	ACCATTTGTGGCCATTCTTCCACCACATTCCGGCTCTTTGGATTTTGGGCTACCAAGCCC	657		
Qy	607	CTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCG	666		
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Qy	667	AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTAC	726		
Db	718	AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTCCAGGAGCCAATGGGACATGCAGTCTAC	777		
Qy	727	ATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCT	786		
Db	778	ATTTGACAACACCATCAAGGAGCATTTCCAGAAGGCTCTAGGCCAGTTTGTCTCATCT	837		

Qy	787	TCTACTGAAAGCAGAGTTGTGGTTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACC	846
Db	838	TCTACTGAAAGCAGAGTTGTGGTTTGTAACTCTGATTTTGCTTTGATTTTGCCCCGCC	897
Qy	847	TCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACC	906
Db	898	CCTGCTTCCCAACACTGTTTATATTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACC	957
Qy	907	ACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTT	966
Db	958	ACAAGACTTGGACAACCTTCATTGCCAAGTTTGGGGATGCAGGGTTTGTCTTGTGGCCTT	1017
Qy	967	GGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTT	1026
Db	1018	TGGCTCCATGTTGAACACCCATCAGTCCCAGGAAGTCCTCAAGAAGATGCACAATGCCTT	1077
Qy	1027	TGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAAAGATGT	1086
Db	1078	TGCCACCTCCCTCAAGGAGTGATATGGACATGTCAGAGTTCTCATTGGCCCAGAGATGT	1137
Qy	1087	CCACCTGGCTGCAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCA	1146
Db	1138	TCATTTGGCCACAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCA	1197
Qy	1147	CCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCA	1206
Db	1198	CCCCAGCATCCGTCTTTTGTCACTCATGGTGGGCAGAACAGCGTAATGGAGGCCATCCG	1257
Qy	1207	GCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCG	1266
Db	1258	TCATGGTGTGCCCATGGTGGGATTACAGTCAATGGAGACCAGCATGGAAAACATGGTCCG	1317
Qy	1267	AGTAGAAGCCAAAAAGTTTGGTGTCTATTAGTTAAAGAAGCTCAAGGCAGAGACATT	1326
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Qy	1447	CCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTG	1506
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Qy	1507	GCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCT	1566
Db	1558	GCATGAGCAGTACCTCATTGATGTCTTTGTGTTTCTGCTGGGGCTCACTCTGGGCACTAT	1617
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Qy 1627 GAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGG 1662
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 Db 1678 GAAGAAGACATGAGGCTAGGTGTAGCCTTGGGTGAG 1713

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Qy	367	TTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCA	426
Db	457	ATTGGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAAATATTTGGGACTCA	516
Qy	427	GTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAACTTCGA	486
Db	517	ATGTAGTTATTTGCTAAGCAGAAAGGATATAATGGATTCCCTTAAAGAATGAGAACTGTGA	576
Qy	487	CATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAA	546
Db	577	TCTGGTATTTGTTGAAGCATTTGATTTCTGTTCTTTCCTGATTGCTGAGAAGCTTGTGAA	636
Qy	547	GCCATTTGTGGCCATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACCAATCCC	606
Db	637	ACCATTTGTGGCCATTCTTCCCACCACATTCCGGCTCTTTGGATTTTGGGCTACCAAGCCC	696
Qy	607	CTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCG	666
Db	697	CTTGTCTTATGTTCCAGTATTCCCTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCG	756
Qy	667	AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTAC	726
Db	757	AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTCCAGGAGCCAATGGGACATGCAGTCTAC	816
Qy	727	ATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCT	786
Db	817	ATTTGACAACACCATCAAGGAGCATTTCCCAGAAGGCTCTAGGCCAGTTTGTCTCATCT	876
Qy	787	TCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACC	846
Db	877	TCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGATTTTGCCTTTGATTTTGCCGGCC	936
Qy	847	TCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACC	906
Db	937	CCTGCTTCCCAACACTGTTTATATTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACC	996
Qy	907	ACAAGACTTGGGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGTGACCTT	966
Db	997	ACAAGACTTGGGAACTTCATTGCCAAGTTTGGGGATGCAGGGTTTGTCTTGTGGCCTT	1056
Qy	967	GGGCTCCATGGTGAACACCTGTCAGAATCCGAAAATCTTCAAGGAGATGAACAATGCCTT	1026
Db	1057	TGGCTCCATGTTGAACACCCATCAGTCCCAGGAAGTCCCTCAAGAAGATGCACAATGCCTT	1116
Qy	1027	TGCTCACCTACCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAAAGATGT	1086
Db	1117	TGCCACCTCCCTCAAGGAGTGATATGGACATGTCAGAGTTCTCATTTGGCCAGAGATGT	1176
Qy	1087	CCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCCTCAGAGTGACCTCCTGGCTCA	1146
Db	1177	TCATTTGGCCACAAATGTGAAAATTGTGGACTGGCTTCCCTCAGAGTGACCTCCTGGCTCA	1236
Qy	1147	CCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCA	1206

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2823)
AUTHORS Isogai,T., Otsuki,T. and Sugiyama,T.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/clone="SMINT1000016"
/tissue_type="small intestine"
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/note="cloning vector: pME18SFL3"
CDS 158. .1729
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ORIGIN

Query Match 55.2%; Score 1281.6; DB 9; Length 2823;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1422; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

Qy 7 CCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTTAGAAAGTGAG 66
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Qy 67 CATGGCTGGGCAGCGAGTGCTTCTTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTCTC 126
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Db 157 CATGGTTGGGCAGCGGGTGCTTCTTAGTGGCCTTCCTTCTTTCTGGGGTCCTGCTCTC 216
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Qy	667	AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTAC	726
Db	757	AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTCCAGGAGCCAATGGGACATGCAGTCTAC	816
Qy	727	ATTTGACAACACCATCAAGGAACATTTACAGAAAGGCTCTAGGCCAGTTTTGTCTCATCT	786
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Qy	787	TCTACTGAAAGCAGAGTTGTGGTTCATTAACCTGACTTTGCCTTTGATTTTGTCTCGACC	846
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Db	997	ACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGATGCAGGGTTTGTCTTGTGGCCTT	1056
Qy	967	GGGCTCCATGGTGAACACCTGTCAGAATCCGAAATCTTCAAGGAGATGAACAATGCCTT	1026
Db	1057	TGGCTCCATGTTGAACACCCATCAGTCCCAGGAAGTCCTCAAGAAGATGCACAATGCCTT	1116
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RESULT 11

AX327327

LOCUS AX327327 2086 bp DNA linear PAT 07-JAN-2002

DEFINITION Sequence 12 from Patent WO0179468.

ACCESSION AX327327

VERSION AX327327.1 GI:18097873

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Policky,J.L., Hafalia,A., Burford,N., Ring,H.Z., Lal,P.,

Tribouley,C.M., Yao,M.G., Yue,H., Tang,Y.T., Patterson,C., Das,D., Sanjanwala,M.S., Gandhi,A.R., Reddy,R., Khan,F.A., Baughn,M.R., Ramkumar,J., Griffin,J.A. and Au-Young,J.

TITLE Drug metabolizing enzymes

JOURNAL Patent: WO 0179468-A 12 25-OCT-2001;
Incyte Genomics, Inc. (US)

FEATURES Location/Qualifiers
source 1. .2086
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/note="Incyte ID No: 2516747CB1"

ORIGIN

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Best Local Similarity 85.8%; Pred. No. 0;
Matches 1421; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

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Qy	1387	CAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGA	1446
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RESULT 12

AX359923

LOCUS AX359923 1572 bp DNA linear PAT 13-FEB-2002

DEFINITION Sequence 3 from Patent WO0202774.

ACCESSION AX359923

VERSION AX359923.1 GI:18675565

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Leiby,K.R., Cook,W.J. and Spaltmann,F.

TITLE 32626, a human udp-glycosyltransferase and uses thereof

JOURNAL Patent: WO 0202774-A 3 10-JAN-2002;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES

source

Location/Qualifiers

1. .1572

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 52.2%; Score 1212; DB 6; Length 1572;

Best Local Similarity 85.7%; Pred. No. 1.5e-310;

Matches 1347; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

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Qy	368	TTAGGTGGCAGAGGAAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAG	427
Db	301	TTGGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAATATTTGGGACTCAA	360
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Qy	488	ATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAG	547
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Qy	548	CCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCC	607
Db	481	CCATTTGTGGCCATTCTTCCCACCACATTCGGCTCTTTGGATTTTGGGCTACCAAGCCCC	540
Qy	608	TTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGA	667
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Qy	668	GTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACA	727
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Qy	728	TTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTT	787
Db	661	TTTGACAACACCATCAAGGAGCATTTCCCAGAAGGCTCTAGGCCAGTTTGTCTCATCTT	720
Qy	788	CTACTGAAAGCAGAGTTGTGGTTCATTAACCTGACTTTGCCTTTGATTTTGCTCGACCT	847
Db	721	CTACTGAAAGCAGAGTTGTGGTTTGTAACTCTGATTTTGCTTTGATTTTGCCCGGCCC	780
Qy	848	CTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCA	907
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Qy	908	CAAGACTTGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGTGACCTTG	967
Db	841	CAAGACTTGAGAACTTCATTGCCAAGTTTGGGGATGCAGGGTTGTCTTGTGGCCTTT	900
Qy	968	GGCTCCATGGTGAACACCTGTCAGAAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTT	1027
Db	901	GGCTCCATGTTGAACACCCATCAGTCCCAGGAAGTCTTCAAGAAGATGCACAATGCCTTT	960
Qy	1028	GCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAAGATGTC	1087
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Db 1021 CATTTGGCCACAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC 1080
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 Db 1081 CCCAGCATCCGTCTTTTTGTCACTCATGGTGGGCAGAACAGCGTAATGGAGGCCATCCGT 1140
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 Qy 1508 CATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTA 1567
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 Db 1441 CATGAGCAGTACCTCATTGATGTCTTTGTGTTTCTGCTGGGGCTCACTCTGGGCATATG 1500
 Qy 1568 TGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTG 1627
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 Db 1501 TGGCTTTGTGGGAAGCTGCTGGGTGTGGTGGCCAGGTGGCTGCGTGGGGCCAGGAAGGTG 1560
 Qy 1628 AAGGAGACATAA 1639
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 Db 1561 AAGAAGACATGA 1572

RESULT 13

AC008947/c

LOCUS AC008947 88948 bp DNA linear HTG 05-MAY-2000
 DEFINITION Homo sapiens chromosome 5 clone CTD-2330L9, WORKING DRAFT SEQUENCE,
 19 unordered pieces.
 ACCESSION AC008947
 VERSION AC008947.5 GI:7710868
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 88948)
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 5
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 88948)
 AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission
 JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT On May 5, 2000 this sequence version replaced gi:6997051.
 -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: <http://www.jgi.doe.gov>

 Project Information
 Center Project Name: 754542
 Center clone name: CITB-H1_2330L9

 Summary Statistics
 Consensus quality: 67454 bases at least Q40
 Consensus quality: 80777 bases at least Q30
 Consensus quality: 83103 bases at least Q20
 Estimated insert size: 85000; pulse field gel estimation
 Estimated insert size: 87148; sum-of-contigs estimation
 Quality coverage: 3.94 in Q20 bases; pulse field gel estimation
 Quality coverage: 3.84 in Q20 bases; sum-of-contigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 19 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 2375: contig of 2375 bp in length
 * 2376 2475: gap of unknown length
 * 2476 5577: contig of 3102 bp in length
 * 5578 5677: gap of unknown length
 * 5678 7838: contig of 2161 bp in length
 * 7839 7938: gap of unknown length
 * 7939 10123: contig of 2185 bp in length
 * 10124 10223: gap of unknown length
 * 10224 12755: contig of 2532 bp in length
 * 12756 12855: gap of unknown length
 * 12856 15242: contig of 2387 bp in length
 * 15243 15342: gap of unknown length
 * 15343 17589: contig of 2247 bp in length
 * 17590 17689: gap of unknown length
 * 17690 20485: contig of 2796 bp in length
 * 20486 20585: gap of unknown length
 * 20586 23628: contig of 3043 bp in length
 * 23629 23728: gap of unknown length
 * 23729 26745: contig of 3017 bp in length
 * 26746 26845: gap of unknown length
 * 26846 30194: contig of 3349 bp in length
 * 30195 30294: gap of unknown length
 * 30295 34563: contig of 4269 bp in length
 * 34564 34663: gap of unknown length
 * 34664 39707: contig of 5044 bp in length
 * 39708 39807: gap of unknown length
 * 39808 47134: contig of 7327 bp in length
 * 47135 47234: gap of unknown length

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*      47235      52767: contig of 5533 bp in length
*      52768      52867: gap of unknown length
*      52868      59030: contig of 6163 bp in length
*      59031      59130: gap of unknown length
*      59131      65592: contig of 6462 bp in length
*      65593      65692: gap of unknown length
*      65693      75313: contig of 9621 bp in length
*      75314      75413: gap of unknown length
*      75414      88948: contig of 13535 bp in length.

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ORIGIN

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Best Local Similarity 99.6%;  Pred. No. 1.1e-242;
Matches 960;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

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Qy      1357 CAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAG 1416
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Db      4584 CAACAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAG 4525

Qy      1417 CCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCA 1476
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Db      4524 CCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCA 4465

Qy      1477 CCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGT 1536
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Db      4464 CCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGT 4405

Qy      1537 GTTCTGCTGGGGCTCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGC 1596
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Db      4404 GTTCTGCTGGGGCTCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGC 4345

Qy      1597 TGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTG 1656
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4344 TGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTG 4285

Qy      1657 GCGGGGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCA 1716
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Qy      1717 GCCCCATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCC 1776
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Qy      1777 AAAAAATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCT 1836
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Db      4164 AAAAAATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCT 4105

Qy      1837 GCTAGCAGAAATCTTTCCAGTCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATG 1896
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Db	4044	CTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATC	3985
Qy	1957	CACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCA	2016
Db	3984	CACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCA	3925
Qy	2017	GACCTAGTCAGCCTCTCTCACTCCTGCCCCCTACTATCTATCATGGAATAACATCCAAGAA	2076
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Db	3864	AGACACCTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCT	3805
Qy	2137	CAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACA	2196
Db	3804	CAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACA	3745
Qy	2197	TTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGAC	2256
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Qy	2257	TGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA	2316
Db	3684	TGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA	3625
Qy	2317	CTAA	2320
Db	3624	CTAA	3621

RESULT 14

AC016612

LOCUS AC016612 179513 bp DNA linear PRI 06-SEP-2001

DEFINITION Homo sapiens chromosome 5 clone CTD-2197M16, complete sequence.

ACCESSION AC016612

VERSION AC016612.6 GI:15451670

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 179513)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 179513)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 179513)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

Db	48440	GCCCCATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCC	48499
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Qy	1837	GCTAGCAGAAATCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATG	1896
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Qy	1897	CTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATC	1956
Db	48620	CTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATC	48679
Qy	1957	CACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCA	2016
Db	48680	CACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCA	48739
Qy	2017	GACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAA	2076
Db	48740	GACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAA	48799
Qy	2077	AGACACCTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCT	2136
Db	48800	AGACACCTTGCATATTCTTTTCAGTTTCTGTTTTGTTCTCCACATATTCTCTTCAATGCT	48859
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Qy	2197	TTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGAC	2256
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Qy	2257	TGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA	2316
Db	48980	TGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA	49039
Qy	2317	CTAA	2320
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RESULT 15

AX155213

LOCUS AX155213 1569 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 3 from Patent WO0138505.

ACCESSION AX155213

VERSION AX155213.1 GI:14536692

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Adler,D.A., Dong,D.L., Pownder,S., Gao,Z. and Conklin,D.C.

TITLE Secreted protein, zalpha37

JOURNAL Patent: WO 0138505-A 3 31-MAY-2001;

	ZymoGenetics, Inc. (US)
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ORIGIN

Query Match 40.7%; Score 944.8; DB 6; Length 1569;
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Matches 822; Conservative 343; Mismatches 403; Indels 0; Gaps 0;

Qy	68	ATGGCTGGGCAGCGAGTGTCTTCTCTAGTGGGCTTCCTTCTCCCTGGGGTCTGCTCTCA	127
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Qy	128	GAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGAC	187
Db	61	GARGCNGCNAARATHYTNACNATHWSNACNYTNGGNGGNWSNCAYTAYTYNYTNYTNNGAY	120
Qy	188	CGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGA	247
Db	121	MGNGTNWSNCARATHYTNCARGARCAYGGNCAYAAAGTNACNATGYTNCAYCARWSNGGN	180
Qy	248	GGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTT	307
Db	181	AARTTYTNYTNATHCCNGAYATHAARGARGARGARAARWSNTAYCARGTNATHMGNTGGTTY	240
Qy	308	GCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGAAGAACT	367
Db	241	WSNCCNGARGAYCAYCARAARMGNATHAARAARCAITTYGAYWSNTAYATHGARACNGCN	300
Qy	368	TTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAG	427
Db	301	YTNGAYGGNMGNAARGARWSNGARGCNYTNGTNAARYTNATGGARATHTTYGGNACNCAR	360
Qy	428	TGCAGTCATTTTTTTAAATAGAAAGGATATCATGGATTCTTTAAAGAATGAGAACTTCGAC	487
Db	361	TGYWSNTAYTYNYTNWSNMGNAARGAYATHATGGAYWSNYTNAARAAYGARAAYTAYGAY	420
Qy	488	ATGGTGATAGTTGAAACTTTTGACTACTGTCTTTCTGATTGCTGAGAAGCTTGGGAAG	547
Db	421	YTNGTNTTYGTNGARGCNTTYGAYTTYTGYSNTTYTNYTNATHGCNGARAARYTNGTNAAR	480
Qy	548	CCATTTGTGGCCATTCTTTCCACTTCATTGGCTCTTTGGAATTTGGGCTACCAATCCCC	607
Db	481	CCNTTYGTNGCNATHYTNCNACNACNTTYGGNWSNYTNGAYTTYGGNYTNCCNWSNCCN	540
Qy	608	TTGTCTTATGTTCCAGTATCCGTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGA	667
Db	541	YTNWSNTAYGTNCCNGTNTTYCCNWSNYTNYTNACNGAYCAYATGGAYTTYTGGGGNMGN	600
Qy	668	GTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACA	727
Db	601	GTNAARAAYTTYTNYTNATGTTYTTYWSNTTYWSNMGNWSNCARTGGGAYATGCARWSNACN	660

QY	728	TTTGACAACACCATCAAGGAACATTTACAGAAAGGCTCTAGGCCAGTTTGTCTCATCTT	787
Db	661	TTYGAYAAYACNATHAARGARCAYYTYCCNGARGGNWSNMGNCNGTNYTNWSNCAYYTN	720
QY	788	CTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGTCTCGACCT	847
Db	721	YTNYTNAARGCNGARYTNTGGTTYGTNAAYWSNGAYTTYGCNTTYGAYTTYGCNMGNCN	780
QY	848	CTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCA	907
Db	781	YTNYTNCNAAYACNGTNTAYATHGGNGGNYTNATGGARAARCCNATHAARCCNGTNCCN	840
QY	908	CAAGACTTGGAAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTG	967
Db	841	CARGAYYTNGAYAAYYTYATHGCNAAYTTYGGNGAYGCNGGNTTYGTNYTNGTNGCNTTY	900
QY	968	GGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTT	1027
Db	901	GGNWSNATGYTNAAYACNCAYCARWSNCARGAGTNYTNAAARAATGCAYAAYGCNTTY	960
QY	1028	GCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAAGATGTC	1087
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QY	1088	CACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC	1147
Db	1021	CAYYTNGCNACNAAYGTNAARATHGTNGAYTGGYTNCNCARWSNGAYYTNYTNGCNCA	1080
QY	1148	CCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAG	1207
Db	1081	CCNWSNATHMGNYTNTTYGTNACNCAYGGNGGNCARAAYWSNGTNATGGARGCNATHMGN	1140
QY	1208	CATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGA	1267
Db	1141	CAYGGNGTNCCNATGGTNGGNYTNCCNGTNAAYGGNGAYCARCAYGGNAAATGGTNMGN	1200
QY	1268	GTAGAAGCCAAAAAGTTTGGTGTCTTCTATTCAAGTAAAGAAGCTCAAGGCAGAGACATTG	1327
Db	1201	GTNGTNGCNAAARAAYTAYGGNGTNWSNATHMGNYTNAAYCARGTNACNGCNGAYACNYTN	1260
QY	1328	GCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCC	1387
Db	1261	ACNYTNACNATGAARCARGTNATHGARGAYAARMGNTAYAARWSNCGNGTNGTNGCNGCN	1320
QY	1388	AGTGTCTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGAC	1447
Db	1321	WSNGTNATHYTNCAYSNCARCCNYTNWSNCCNGCNCARMGNYTNGTNGGNTGGATHGAY	1380
QY	1448	CACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTAGCAGCCCTGG	1507
Db	1381	CAYATHYTNCARACNGGNGGNGCNACNAYYTNAARCCNTAYGCNTTYCARCARCCNTGG	1440
QY	1508	CATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTTCTGCTGGGGCTCACTCTGGGGACTCTA	1567
Db	1441	CAYGARCARTAYYTNAATHGAYGTNTTYGTNTTYTNYTNGGNYTNACNYTNGGNACNATG	1500
QY	1568	TGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTG	1627

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Db      1501 TGGYTNTGYGGNAARYTNYTNGGNGTNGTNGCNMGNTGGYTNTMGNGGNGCNMGNAARGTN 1560
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 3373863 seqs, 2124099041 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2320	100.0	2320	8	ACD68440	Acd68440 Novel hum
5	2320	100.0	2320	8	ACH04542	Ach04542 Human cDN
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12	2320	100.0	2320	9	ADD39396	Add39396	Human	cDN
13	2320	100.0	2320	9	ADD38919	Add38919	Human	cDN
14	2320	100.0	2320	9	ADD40350	Add40350	Human	cDN
15	2320	100.0	2320	9	ADE50571	Ade50571	Human	cDN
16	2320	100.0	2320	9	ADE20183	Ade20183	Human	cDN
17	2320	100.0	2320	9	ADE50094	Ade50094	Human	cDN
18	2320	100.0	2320	9	ADE21652	Ade21652	Human	cDN
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20	2102.8	90.6	2944	6	AAL41485	Aal41485	Drug	meta
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c 35	708.2	30.5	1898	4	ABA09537	Aba09537	Human	PRO
36	595.2	25.7	770	5	AAF93971	Aaf93971	Primer	sp
37	593.4	25.6	1842	9	ADB62657	Adb62657	Human	cDN
c 38	538.4	23.2	594	5	AAF94120	Aaf94120	Primer	sp
39	487.6	21.0	2220	5	AAS81804	Aas81804	DNA	encod
40	433.6	18.7	42999	6	ABK90832	Abk90832	Genomic	D
c 41	399.6	17.2	659	5	AAS81803	Aas81803	DNA	encod
42	319.6	13.8	923	4	AAS41046	Aas41046	cDNA	enco
43	319.4	13.8	981	4	AAS41586	Aas41586	cDNA	enco
44	319.4	13.8	981	4	AAL01667	Aal01667	Human	rep
45	239.2	10.3	5973	4	AAL05664	Aal05664	Human	rep

ALIGNMENTS

RESULT 1

AAC58107

ID AAC58107 standard; cDNA; 2320 BP.

XX

AC AAC58107;

XX

DT 25-JAN-2001 (first entry)

XX

DE Human PRO1780 nucleotide sequence SEQ ID NO:12.

XX

KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
KW identification; tumourigenesis; anticancer; detection; ss.

XX

OS Homo sapiens.

XX
 PN WO200053750-A1.
 XX
 PD 14-SEP-2000.
 XX
 PF 02-DEC-1999; 99WO-US028551.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028634.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
 XX
 DR WPI; 2000-594320/56.
 DR P-PSDB; AAB24025.
 XX
 PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit
 PT the growth of tumors in mammals, and to identify inhibitors of PRO
 PT polypeptide activity or expression.
 XX
 PS Claim 50; Fig 9; 226pp; English.
 XX
 CC The present invention describes an antibody that binds to a human protein
 CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
 CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
 CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
 CC activity and can be used to diagnose tumours in mammals, by detecting
 CC complex formation when the antibody is contacted with test cells.
 CC Increased expression of genes encoding (I) can also be detected to
 CC diagnose tumours. Agents which inhibit the activity of (I), especially
 CC the antibodies, or an antisense oligonucleotide which hybridises to genes
 CC encoding (I), can be used to inhibit tumour growth, preferably by
 CC inducing cell death. Methods from the present invention can be used to
 CC identify compounds which inhibit the biological activity of (I). AAC58019
 CC to AAC58102 represent PCR primers and hybridisation probes used in
 CC examples from the present invention for human PRO sequences. AAC58103 to
 CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
 CC protein sequences given in the exemplification of the present invention
 XX
 SQ Sequence 2320 BP; 545 A; 581 C; 538 G; 656 T; 0 U; 0 Other;

 Query Match 100.0%; Score 2320; DB 3; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120

Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTGGAAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTGGAAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020

Db	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Qy	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381		GGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381		GGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441		GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441		GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501		GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501		GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561		GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561		GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621		AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621		AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681		TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681		TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741		TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Db	1741		TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Qy	1801		ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860

Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 2

AAA37101

ID AAA37101 standard; cDNA; 2320 BP.

XX

AC AAA37101;

XX

DT 08-AUG-2000 (first entry)

XX

DE Human PRO1780 (UNQ842) cDNA sequence SEQ ID NO:281.

XX

KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.

XX

OS Homo sapiens.

XX

PN WO200012708-A2.

XX

PD 09-MAR-2000.

XX

PF 01-SEP-1999; 99WO-US020111.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.

PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.

PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.

PA (GETH) GENENTECH INC.

PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;

DR WPI; 2000-237871/20.

DR P-PSDB; AAY99419.

PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.

PS Claim 2; Fig 159; 773pp; English.

CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention

SQ Sequence 2320 BP; 545 A; 581 C; 538 G; 656 T; 0 U; 0 Other;

Query Match 100.0%; Score 2320; DB 3; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
 |||
 Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
|||||

Db 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy 121 GCTCTCAGAGGCTGCCAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
 |||
 Db 121 GCTCTCAGAGGCTGCCAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy 241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
 |||
 Db 241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200

Db	1141	 GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	 GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	 GATTGACCACGTCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	 CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040

Db 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
 Qy 2041 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
 |||||
 Db 2041 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
 Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
 |||||
 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
 Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
 |||||
 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
 Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
 |||||
 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
 |||||
 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 3

AAF54401

ID AAF54401 standard; DNA; 2320 BP.
 XX
 AC AAF54401;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Primer #82 used in the identification of proteins.
 XX
 KW Secreted; transmembrane; gene therapy; ss.
 XX
 OS Unidentified.
 XX
 PN WO200078961-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 18-FEB-2000; 2000WO-US004342.
 XX
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

XX

DR WPI; 2001-071395/08.

XX

PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.

XX

PS Example 82; Page 456; 787pp; English.

XX

CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy

XX

SQ Sequence 2320 BP; 545 A; 581 C; 538 G; 656 T; 0 U; 0 Other;

Query Match 100.0%; Score 2320; DB 4; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
QY	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
QY	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
QY	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
QY	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
QY	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
QY	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
QY	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480

Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTGTGGCCATTCTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTGTGGCCATTCTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320

Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCAGTCTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCAGTCTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220

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Db      2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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Qy      2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
      |||
Db      2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
      |||
Qy      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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Db      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

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RESULT 4

ACD68440

ID ACD68440 standard; cDNA; 2320 BP.

XX

AC ACD68440;

XX

DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1780 cDNA.

XX

KW Human; secreted and transmembrane protein; PRO; angiogenesis;
 KW endothelial cell proliferation; wound healing; immune response;
 KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
 KW cardiac insufficiency disorder; calcium flux; inflammation;
 KW vascular endothelial growth factor-stimulated proliferation;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
 KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia;
 KW pancreatic beta-cell precursor cell differentiation; thalassemias;
 KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
 KW cartilage disorder; sports injury; arthritis; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003073130-A1.

XX

PD 17-APR-2003.

XX

PF 11-DEC-2001; 2001US-00015869.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

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PR 01-OCT-1998; 98US-0102684P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
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PR 10-NOV-1998; 98US-0107783P.
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PR 18-NOV-1998; 98US-0108848P.
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PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

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PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;

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DR WPI; 2003-585293/55.

DR P-PSDB; ABO33661.

XX

PT Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
 PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
 PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

Query Match 100.0%; Score 2320; DB 8; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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 Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
 QY 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
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 Db 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
 QY 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Db	121		GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181		GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181		GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241		CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241		CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301		TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301		TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361		AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361		AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421		GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Db	421		GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Qy	481		CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481		CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601		AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601		AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAAGGCTCTAGGCCAGTTTGTG	780
Db	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAAGGCTCTAGGCCAGTTTGTG	780
Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020

Db 961 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA 1020
 Qy 1021 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCACTGTTCTCATTGGCCCAA 1080
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1021 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCACTGTTCTCATTGGCCCAA 1080
 Qy 1081 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT 1140
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 Db 1081 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT 1140
 Qy 1141 GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC 1200
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 Db 1141 GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC 1200
 Qy 1201 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1260
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 Db 1201 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1260
 Qy 1261 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA 1320
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 Qy 1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380
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 Db 1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380
 Qy 1381 GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440
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 Db 1381 GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440
 Qy 1441 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500
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 Db 1441 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500
 Qy 1501 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560
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 Db 1501 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560
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 Qy 1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680
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 Qy 1681 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1740
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 Qy 1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT 1860
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Qy 1861 CTTGTCCTCCTTTGTTTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
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 Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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 Db 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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 Qy 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
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 Db 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
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 Qy 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCACT 2100
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 Db 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCACT 2100
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 Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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 Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
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 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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RESULT 5

ACH04542

ID ACH04542 standard; cDNA; 2320 BP.

XX

AC ACH04542;

XX

DT 01-OCT-2003 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; vulnerary;
 KW cardiant; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
 KW adrenal cortical capillary; endothelial cell growth; wound healing;
 KW stimulated T-lymphocyte proliferation; immune response suppression;
 KW neonatal heart hypertrophy; cardiac insufficiency disorder;
 KW vascular endothelial growth factor; inflammation; mononuclear cell;
 KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
 KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
 KW sports injury; arthritis.

XX

OS Homo sapiens.

XX

PN US2003044841-A1.

XX
PD 06-MAR-2003.
XX
PF 06-DEC-2001; 2001US-00006856.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
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PR 15-SEP-1998; 98US-0100388P.
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PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
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PR 03-NOV-1998; 98US-0106919P.
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PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.

PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
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PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
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PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

XX
DR WPI; 2003-492259/46.
DR P-PSDB; ABO44514.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating various cardiac insufficiency
PT disorders, bone and/or cartilage disorders such as sports injuries and
PT arthritis.

Query Match 100.0%; Score 2320; DB 8; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
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Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCACTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCACTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660

Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCAACCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCAACCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTAGCA	1500
Db	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560

Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTTCTAGGGAGCTTCCCAGTCTGCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Db	1801	 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	 CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Db	2221	 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

ACD68086

ID ACD68086 standard; cDNA; 2320 BP.

XX

AC ACD68086;

XX

DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1780 cDNA.

XX

KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
KW tissue typing; chromosome identification; vaccine; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003073129-A1.

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PD 17-APR-2003.

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PF 04-SEP-2001; 2001US-00946374.

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 Db 481 CTTGCACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
 Qy 541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
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 Db 601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG 660
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Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
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Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040

Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
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Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
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RESULT 7

ADC18150

ID ADC18150 standard; cDNA; 2320 BP.

XX

AC ADC18150;

XX

DT 18-DEC-2003 (first entry)

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DE Human PRO polynucleotide #80.

XX

KW Human; PRO; gene; ss; protein electrophoresis; chromosome mapping;

KW gene mapping; genetic disorder.

XX

OS Homo sapiens.

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PN US2003064925-A1.

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PD 03-APR-2003.

XX

PF 10-DEC-2001; 2001US-00013907.

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XX

PA (GETH) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

XX

DR WPI; 2003-555602/52.

DR P-PSDB; ADC18151.

XX

PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.

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PS Claim 2; SEQ ID NO 281; 555pp; English.

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CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The sequences are useful in the preparation of a
CC medicament for treating a condition responsive to a PRO polypeptide. The
CC polypeptides are useful in a number of functional biological assays, as
CC molecular weight markers for protein electrophoresis and as therapeutic

Query Match 100.0%; Score 2320; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900

Db	841	 TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	 GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Db	1021	 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	 GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	 GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740

Db	1681	TCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 8

ADD70796

ID ADD70796 standard; cDNA; 2320 BP.

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AC ADD70796;

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DT 15-JAN-2004 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003099625-A1.
XX
PD 29-MAY-2003.
XX
PF 12-DEC-2001; 2001US-00015386.
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PR 10-NOV-1998; 98US-0107783P.
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PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
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Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380

Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280

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Db      2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280

QY      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
      ||||||||||||||||||||||||||||||||||||||||||||
Db      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

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RESULT 9

ADD39873

ID ADD39873 standard; cDNA; 2320 BP.

XX

AC ADD39873;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003083462-A1.

XX

PD 01-MAY-2003.

XX

PF 10-DEC-2001; 2001US-00013913.

XX

PR 05-JAN-1999; 99WO-US000106.

PR 01-SEP-1999; 99WO-US020111.

PR 15-SEP-1999; 99WO-US021194.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004342.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 15-MAR-2000; 2000WO-US006884.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2003-755122/71.
 DR P-PSDB; ADD39874.
 XX
 PT New secreted and transmembrane PRO polypeptides useful for treating
 PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
 PT hypo-insulinemia, sports injuries and arthritis.
 XX
 PS Claim 2; SEQ ID NO 281; 557pp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (secreted or
 CC transmembrane protein) having at least 80% amino acid sequence identity
 CC to an amino acid sequence chosen from 123 fully defined sequences as
 CC given in the specification (including their extracellular domains either
 CC or without their associated signal peptides. Also include are the
 CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
 CC host cell comprising the vector, producing PRO, a chimaeric molecule
 CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
 CC PRO antibody. Pro is useful as molecular weight markers for protein
 CC electrophoresis and also for chromosome identification. PRO is also
 CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
 CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
 CC useful for generating transgenic animals or knock-out animals which are
 CC useful in development and screening useful reagents. PRO NA is also
 CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
 CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
 CC polypeptides are useful for suppressing immune response. PRO1246
 CC polypeptide is useful for treating cardiac insufficiency disorders.
 CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
 CC PRO1561 polypeptide are useful for stimulating calcium flux in human
 CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
 CC polypeptides are useful for treating bone and/or cartilage disorders
 CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
 CC polypeptides are useful for treating diabetes in skeletal muscle cells
 CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
 CC treating Berger disease or other nephropathies associated with Schonlein-
 CC Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's
 CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
 CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
 CC sequence encodes a PRO protein of the invention.
 XX
 SQ Sequence 2320 BP; 545 A; 581 C; 538 G; 656 T; 0 U; 0 Other;

 Query Match 100.0%; Score 2320; DB 9; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60
      |||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
      |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
      |||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
      |||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 300
      |||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
      |||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
      |||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTTAAAGAATGAGAA 480
      |||
Db    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTTAAAGAATGAGAA 480

Qy    481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
      |||
Db    481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600
      |||
Db    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600

Qy    601 AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660
      |||
Db    601 AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660

Qy    661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
      |||
Db    661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720

Qy    721 GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC 780
      |||
Db    721 GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC 780

Qy    781 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC 840
      |||
Db    781 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC 840
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Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCTCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTAGCA	1500
Db	1441	GATTGACCACGTCCTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680

Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 10

ADD70319

ID ADD70319 standard; cDNA; 2320 BP.

XX

AC ADD70319;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.
 XX
 OS Homo sapiens.
 XX
 PN US2003054406-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 06-DEC-2001; 2001US-00006818.
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 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099596P.
 PR 09-SEP-1998; 98US-0099598P.
 PR 09-SEP-1998; 98US-0099602P.
 PR 09-SEP-1998; 98US-0099642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099808P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 10-SEP-1998; 98US-0099816P.
 PR 15-SEP-1998; 98US-0100385P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
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 PR 16-SEP-1998; 98US-0100664P.
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 PR 23-SEP-1998; 98US-0101474P.
 PR 23-SEP-1998; 98US-0101475P.

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PR	23-SEP-1998;	98US-0101479P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101741P.
PR	24-SEP-1998;	98US-0101743P.
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PA (GETH) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

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DR WPI; 2003-708344/67.

DR P-PSDB; ADD70320.

XX

PT Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.

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PS Claim 2; SEQ ID NO 281; 549pp; English.

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CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2320; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
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Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCCTTTCCTGATTGCTGAGAAGCT	540

Db	481		CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTCTCTGATTGCTGAGAAGCT	540
Qy	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
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Qy	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
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Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
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Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
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Qy	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
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Qy	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
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Qy	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
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Qy	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
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Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
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Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
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Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
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Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
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Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
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 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 11

ADD38440

ID ADD38440 standard; cDNA; 2320 BP.

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AC ADD38440;

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DT 15-JAN-2004 (first entry)

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DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

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OS Homo sapiens.

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PN US2003096955-A1.

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PD 22-MAY-2003.

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PF 07-DEC-2001; 2001US-00012755.

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PR      18-FEB-2000; 2000WO-US004342.
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PR      08-NOV-2000; 2000WO-US030952.
PR      10-NOV-2000; 2000WO-US030873.
PR      01-DEC-2000; 2000WO-US032678.
PR      28-FEB-2001; 2001WO-US006520.
PR      01-MAR-2001; 2001WO-US006666.
PR      01-JUN-2001; 2001WO-US017800.
PR      20-JUN-2001; 2001WO-US019692.
PR      29-JUN-2001; 2001WO-US021066.
PR      09-JUL-2001; 2001WO-US021735.
PR      04-SEP-2001; 2001US-00946374.
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PA (GETH) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

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DR WPI; 2003-787000/74.

DR P-PSDB; ADD38441.

XX

PT Novel isolated PRO polypeptide, useful for treating cancerous tumors,
PT cardiac insufficiency disorders, wound healing, diabetes mellitus,
PT thalassemias.

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PS Claim 2; SEQ ID NO 281; 556pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity

Query Match 100.0%; Score 2320; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180

Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020

Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGT CAGTGTTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGT CAGTGTTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGT CACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGT CACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATT CAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATT CAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGT CATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGT CATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTT CAGCA	1500
Db	1441	GATTGACCACGTCTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTT CAGCA	1500
Qy	1501	GGCCTGGCATGAGCAGTACCTGTTCTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GGCCTGGCATGAGCAGTACCTGTTCTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920

Db	1861	 CTTGTCTCTCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 12

ADD39396

ID ADD39396 standard; cDNA; 2320 BP.

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AC ADD39396;

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DT 15-JAN-2004 (first entry)

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DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

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PN US2003096954-A1.

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PD 22-MAY-2003.

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PF 07-DEC-2001; 2001US-00011671.

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PR 18-NOV-1998; 98US-0108904P.
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PR 05-JAN-1999; 99WO-US000106.
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PR 15-SEP-1999; 99WO-US021194.
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PR 16-DEC-1999; 99WO-US030095.
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PR 11-FEB-2000; 2000WO-US003565.
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PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
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PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
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PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

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PA (GETH) GENENTECH INC.

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PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

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DR WPI; 2003-786999/74.

DR P-PSDB; ADD39397.

XX

PT Novel isolated PRO polypeptide useful for tissue typing, modulating

Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560

Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 13

ADD38919

ID ADD38919 standard; cDNA; 2320 BP.

XX
 AC ADD38919;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.
 XX
 OS Homo sapiens.
 XX
 PN US2003092061-A1.
 XX
 PD 15-MAY-2003.
 XX
 PF 06-DEC-2001; 2001US-00007194.
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PR 24-AUG-2000; 2000WO-US023328.

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Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
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Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAAATCCGGAAATCTTCAAGGAGATGAACAA	1020
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Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGTGATATGGAAGTGTGAGTTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGTGATATGGAAGTGTGAGTTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260

Db	1201	 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
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Db	1261	 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	 GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
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Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTTCTAGGGAGCTTCCCAGTCTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
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Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
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RESULT 14

ADD40350

ID ADD40350 standard; cDNA; 2320 BP.

XX

AC ADD40350;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003082627-A1.

XX

PD 01-MAY-2003.

XX

PF 06-DEC-2001; 2001US-00006117.

XX

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PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.

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PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
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PR 16-DEC-1999; 99WO-US030095.
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PR 02-JUN-2000; 2000WO-US015264.
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PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-755104/71.
DR P-PSDB; ADD40351.
XX
PT New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
PT insufficiency disorders.
XX
PS Claim 2; SEQ ID NO 281; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2320; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTTAGA 60
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 Db 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
 Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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 Db 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
 Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
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 Db 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
 Qy 241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
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 Db 301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
 Qy 361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
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 Db 361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
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Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
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Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATAACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATAACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
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Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
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Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740

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Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGA	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGA	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
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Qy	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCA	2100
Db	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCA	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCC	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCC	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
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RESULT 15

ADE50571

ID ADE50571 standard; cDNA; 2320 BP.

XX

AC ADE50571;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX
OS Homo sapiens.
XX
PN US2003069179-A1.
XX
PD 10-APR-2003.
XX
PF 11-DEC-2001; 2001US-00015393.
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PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
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PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

XX

DR WPI; 2003-708395/67.

DR P-PSDB; ADE50572.

XX

PT Novel secreted and transmembrane PRO polypeptides useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide and as therapeutic agents e.g. vaccines.

XX

PS Claim 2; SEQ ID NO 281; 555pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2320; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
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Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Qy    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
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Db    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600
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Db	541		TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601		AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601		AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901		AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901		AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Db	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Qy	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381		GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440

Db	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280

Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

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Job time : 1309 secs

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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 06:50:49 ; Search time 190 Seconds
(without alignments)
6776.242 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 agggtccttagccgggcgc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
c	1	452.2	19.5	883	4	US-09-833-381-210			Sequence 210, App
c	2	424.2	18.3	1056	4	US-09-833-381-631			Sequence 631, App
	3	382.4	16.5	470	4	US-09-833-381-348			Sequence 348, App
	4	143.2	6.2	2966	4	US-09-976-594-241			Sequence 241, App
	5	136.4	5.9	2107	3	US-09-180-852-1			Sequence 1, Appli
	6	136	5.9	1854	4	US-09-356-806-39			Sequence 39, Appl
	7	131.6	5.7	2092	4	US-09-356-806-7			Sequence 7, Appli
	8	128.4	5.5	1976	4	US-09-356-806-112			Sequence 112, App
	9	127.6	5.5	1413	4	US-09-813-918-1			Sequence 1, Appli
	10	118	5.1	2336	5	PCT-US92-00282-1			Sequence 1, Appli
	11	111.2	4.8	2339	5	PCT-US92-00282-2			Sequence 2, Appli

	12	95.6	4.1	735	4	US-09-305-856B-17	Sequence 17, Appl
	13	79.2	3.4	7218	1	US-08-232-463-14	Sequence 14, Appl
c	14	74	3.2	588	4	US-09-833-381-344	Sequence 344, App
	15	63.8	2.8	689	4	US-09-356-806-5	Sequence 5, Appli
	16	62.4	2.7	391	4	US-09-370-838-21	Sequence 21, Appl
	17	62.2	2.7	1591	4	US-09-356-806-44	Sequence 44, Appl
	18	56.8	2.4	1731	2	US-08-466-583-1	Sequence 1, Appli
	19	56.8	2.4	1731	4	US-08-265-427-1	Sequence 1, Appli
	20	56.8	2.4	1731	5	PCT-US95-07820-1	Sequence 1, Appli
	21	56.2	2.4	983	4	US-09-671-317-386	Sequence 386, App
	22	55	2.4	1602	4	US-09-356-806-117	Sequence 117, App
	23	53.4	2.3	783	5	PCT-US92-00282-22	Sequence 22, Appl
	24	49.2	2.1	657	4	US-09-669-751-104	Sequence 104, App
	25	48.6	2.1	1001	4	US-09-671-317-404	Sequence 404, App
	26	44.6	1.9	762	4	US-09-615-192A-218	Sequence 218, App
	27	43.6	1.9	1001	4	US-09-671-317-413	Sequence 413, App
	28	43.6	1.9	1001	4	US-09-671-317-414	Sequence 414, App
	29	43.6	1.9	1001	4	US-09-671-317-415	Sequence 415, App
	30	43.6	1.9	1001	4	US-09-671-317-417	Sequence 417, App
	31	43.6	1.9	1021	4	US-09-356-806-115	Sequence 115, App
	32	43.2	1.9	1001	4	US-09-671-317-416	Sequence 416, App
	33	42.6	1.8	2025	3	US-08-942-012B-23	Sequence 23, Appl
	34	42	1.8	1800	6	5180581-1	Patent No. 5180581
	35	42	1.8	2793	1	US-08-281-916-5	Sequence 5, Appli
	36	42	1.8	2793	2	US-08-460-725-7	Sequence 7, Appli
c	37	39.8	1.7	289	3	US-09-007-005-17	Sequence 17, Appl
c	38	39.8	1.7	289	3	US-09-244-796-17	Sequence 17, Appl
	39	39.6	1.7	50937	3	US-09-428-517-1	Sequence 1, Appli
	40	39.2	1.7	492	4	US-09-134-001C-808	Sequence 808, App
	41	39	1.7	759	4	US-09-305-856B-15	Sequence 15, Appl
	42	39	1.7	930	4	US-09-305-856B-13	Sequence 13, Appl
	43	39	1.7	1200	1	US-08-096-623A-19	Sequence 19, Appl
	44	38.8	1.7	474	4	US-09-621-976-18033	Sequence 18033, A
	45	38.8	1.7	11049	4	US-10-204-708-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-833-381-210/c

; Sequence 210, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 210

; LENGTH: 883

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(883)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-210

Query Match 19.5%; Score 452.2; DB 4; Length 883;
Best Local Similarity 83.8%; Pred. No. 2.2e-129;
Matches 511; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy      331 ATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGGTGGCAGAGGAAAATTTGA 390
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      881 AATTAAGAAGCATTNTGATAGCTACATAGAAACAGCATTGGATGGCAGAAAAGAATCTGA 822

Qy      391 AAAC TTATTAATGTTCTAGAACTTGGCGTTGCAGTGCAGTCATTTTTTAAATAGAAA 450
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      821 AGCCCTTGTAAGCTAATGGAAATATTTGGGACTCAATGTAGTTATTTGCTAAGCAGAAA 762

Qy      451 GGATATCATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAACTTTTGA 510
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      761 GGATATAATGGATTCCTTAAAGAATGAGAACTATGATCTGGTATTTGTTGAAGCATTGA 702

Qy      511 CTA CTGTCCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCCAC 570
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      701 TTTCTGTTCTTTCTGATTGCTGAGAAGCTTGTGAAACCATTTGTGGCCATTCTTTCCCAC 642

Qy      571 TTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCG 630
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Db      641 CACATTTCGGCTCTTTGGATTTTGGGCTACCAAGCCCCTTGTCTTATGTTCCAGTATTCCC 582

Qy      631 TTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTT 690
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      581 TTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTT 522

Qy      691 TAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACA 750
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Db      521 TAGTTTCTCCAGGAGCCAATGGGACATGCAGTCTACATTTGACAACACCATCAAGGAGCA 462

Qy      751 TTTCACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTT 810
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Db      461 TTTCACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTT 402

Qy      811 CATTA ACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGT 870
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Db      401 TGTTA ACTCTGATTTTGCCCTTTGATTTTGCCCGGCCCTGCTTCCCAACACTGTTTATAT 342

Qy      871 TGGAGGCTTGATGGA AAAACCTATTAAACCAGTACCACAAGACTTGGAGA ACTTCATTGC 930
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      341 TGGAGGCTTGATGGA AAAACCTATTAAACCAGTACCACAAGTAAATAAACAGTTGGCATT 282

Qy      931 CAAGTTTGGG 940
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Db      281 CAGTTTGGG 272
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RESULT 2
US-09-833-381-631/c

RESULT 3

US-09-833-381-348

; Sequence 348, Application US/09833381
 ; Patent No. 6672186
 ; GENERAL INFORMATION:
 ; APPLICANT: Robison, Keith E.
 ; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
 ; FILE REFERENCE: 5800-119
 ; CURRENT APPLICATION NUMBER: US/09/833,381
 ; CURRENT FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: 09/516,448
 ; PRIOR FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 2050
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 348
 ; LENGTH: 470
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(470)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-833-381-348

Query Match 16.5%; Score 382.4; DB 4; Length 470;
 Best Local Similarity 95.9%; Pred. No. 5.6e-108;
 Matches 446; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

Qy	963	CCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATG	1022
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Qy	1023	CCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAAAG	1082
Db	61	CCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCAAAG	120
Qy	1083	ATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGG	1142
Db	121	ATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGG	180
Qy	1143	CTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCA	1202
Db	181	CTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCA	240
Qy	1203	TCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGG	1262
Db	241	TCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGG	300
Qy	1263	TCCGAGTAGAAGCCAAAAAG-TTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAG	1321
Db	301	TCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAG	360
Qy	1322	ACATTGGCTC-TTAAGATGAAACAAATCATGG--AAGACAAGAGATACAAGTCCGC-GGC	1377
Db	361	ACATTGGCTCTTTAAGATGAAACAAATCATGGGAAGGACAAGAGATACAAGTCCGC	420

Qy 1378 AGTGGCT--GCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCC 1420
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 Db 421 AGTGGCTTGCCAGTGTTCNTCCTGCGTTCCCACCCGTTAGGCCC 465

RESULT 4

US-09-976-594-241

; Sequence 241, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 241

; LENGTH: 2966

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. 6673549 997080.1

US-09-976-594-241

Query Match 6.2%; Score 143.2; DB 4; Length 2966;

Best Local Similarity 48.3%; Pred. No. 2.2e-33;

Matches 542; Conservative 0; Mismatches 553; Indels 27; Gaps 4;

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 Db 411 TTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCAACTACGATGTAATGCTT 470
 Qy 497 GTTGAAACTTTTGACTACTGTCCCTTTCCTGATTGCTGAGAAGCTTGGAAGCCATTTGTG 556
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 Db 471 ATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTGTG 530
 Qy 557 GCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGG-----GCTACCAATC 604
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 Db 531 CTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCCAGCT 590
 Qy 605 CCCTTGCTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGC 664
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 Db 591 CCACTTTCCTATGTACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAA 650
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 Db 651 AGAGTAAAAAATCAATGCTTTCAGTTTGTTCCACTTCTGGATTACGACTAT 710
 Qy 725 ACATTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCAT 784
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Qy	785	CTTCTACTGAAAGCAGAGTTGTGGTTCATTAAGTCTGACTTTGCCTTTGATTTTGCTCGA	844
Db	768	ACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCTCTCAA	827
Qy	845	CCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTA	904
Db	828	CCATACCAACCTAAGTTTGTGAGTTTGTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTG	887
Qy	905	CCACAAGACTTGGAGAAGTTTCTATTGCCAAGTTTGGGGACTCTGGTTTGTCTTGTGACC	964
Db	888	CCTAAGGAAATGGAAAATTTGTCCAGAGTTTCAGGGGAAGATGGTATTGTGGTGTCTTCT	947
Qy	965	TTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCC	1024
Db	948	CTGGGGTCACTGTTTCAAATGTTACAGA---AGAAAAGGCTAATATCATTGCTTCAGCC	1004
Qy	1025	TTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAAGAT	1084
Db	1005	CTTGCCCGAGATCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAACCATCCACA---	1061
Qy	1085	GTCCACCTGGCTGCAAATGTGAAAATGTGGACTGGCTTCTCAGAGTGACCTCCTGGCT	1144
Db	1062	-----TTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAATGATCTTCTTGGT	1115
Qy	1145	CACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGCCATC	1204
Db	1116	CATCCCAAAACCAAAGCTTTTATCACTCATGGTGGAATGAATGGGATCTATGAAGCTATT	1175
Qy	1205	CAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTC	1264
Db	1176	TACCATGGGGTCCCTATGGTGGGAGTCCCATATTTGGTGATCAGCTTGATAACATAGCT	1235
Qy	1265	CGAGTAGAAGCCAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACA	1324
Db	1236	CACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAACTATGACAAGCGAAGAT	1295
Qy	1325	TTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCT	1384
Db	1296	TTACTGAGGGCTTTGAGAACAGTCATTACCGATTCTCTTATAAAGAGAATGCTATGAGA	1355
Qy	1385	GCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATT	1444
Db	1356	TTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCTAGATCGAGCAGTCTTCTGGATC	1415
Qy	1445	GACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCC	1504
Db	1416	GAGTTTGTTCATGCGCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCATGACCTCACC	1475
Qy	1505	TGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTG	1546
Db	1476	TGGTTCAGCACTACTCTATAGATGTGATTGGGTTCCTGCTG	1517

```
; Sequence 1, Application US/09180852
; Patent No. 6287834
; GENERAL INFORMATION:
; APPLICANT: BELANGER, Alain
; APPLICANT: HUM, Dean W.
; APPLICANT: BEAULIEU, Martin
; APPLICANT: LEVESQUE, Eric
; TITLE OF INVENTION: CHARACTERIZATION AND USE OF AN ISOLATED URIDINE
; TITLE OF INVENTION: DIPHOSPHO-GLUCURONOSYLTRANSFERASE
; FILE REFERENCE: 1259-449
; CURRENT APPLICATION NUMBER: US/09/180,852
; CURRENT FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: PCT/CA97/00328
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: US 08/649,319
; EARLIER FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(1644)
US-09-180-852-1
```

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Query Match          5.9%; Score 136.4; DB 3; Length 2107;
Best Local Similarity 49.5%; Pred. No. 2.2e-31;
Matches 473; Conservative 0; Mismatches 466; Indels 17; Gaps 4;
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Qy      593 GGGCTACCAATCCCCTTGTCTTATGTTCCAGTATCCGTTCCCTTGCTGACTGATCACATG 652
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      610 GGATTTCTGTTCCTTCCTATGTACCTGTTGTTATGTGAGAATTAAGTGATCAAATG 669

Qy      653 GACTTCTGGGGCCGAGTGAAGAATTTTCT-GATGTTCTTTAGTTTCTGCAGGAGGCAACA 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      670 ATTTTCATGGAGAGGATAAAAAATATGATATATATGCTTTATTTTGACTTTTGGTTTCAA 729

Qy      712 GCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCC 771
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      730 GCATATGATCTGAAGAAGTGGGACCAGTTTTATAGTGAAGTCTAGGAAGACCCACTACA 789

Qy      772 AGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTT 831
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      790 TTATTTGAGACA----ATGGGGAAAGCTGAAATGTGGCTCATTCGAACCTATTGGGATTT 845

Qy      832 TGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACC 891
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      846 TGAATTTCTCGCCCATCTTACCAAATGTTGATTTTGTGGAGGACTTCACTGTAAACC 905

Qy      892 TATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTT 951
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      906 AGCCAAACCTTGCCTAAGGAAATGGAAGAGTTTGTGCAGAGCTCTGGAGAAAATGGTAT 965

Qy      952 TGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGA 1011
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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; SEQ ID NO 39
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)...(1584)
US-09-356-806-39
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Query Match          5.9%; Score 136; DB 4; Length 1854;
Best Local Similarity 49.6%; Pred. No. 2.7e-31;
Matches 469; Conservative 0; Mismatches 460; Indels 17; Gaps 4;
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Qy      603 TCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGG 662
      |||  || || || || ||  |  ||  ||||| |||  |||  ||
Db      580 TCCCTCCTTCCTACGTACCTGTTGTTATGTGAGAATTAAGTATCAAATGACTTTCATGG 639

Qy      663 GCCGAGTGAAGAATTTTCT-GATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAG 721
      | || || || | | ||| |||| |||  |  |  ||
Db      640 AGAGGGTAAAAAATATGATCTATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACA 699

Qy      722 TCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCT 781
      | | | || || || | | | | ||| ||| | |  | |||
Db      700 TGAAGAAGTGGGATCAGTTTTATAGTGAAGTCTAGGAAGACCC-----ACTACATTATCT 755

Qy      782 CATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAGTCTGACTTTGCCTTTGATTTTGCT 841
      |  |  ||||| || | || | |||  ||  ||| | || |
Db      756 GAGACAATGGGGAAAGCTGACGTATGGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCA 815

Qy      842 CGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCA 901
      || || | || || || || ||||| ||  ||||| |||||
Db      816 TATCCACTCTTACCAAATGTTGATTTTGTGGAGGACTCCACTGCAAACCTGCCAAACCC 875

Qy      902 GTACCACAAGACTTGGAGAAGTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGTG 961
      || | || || ||| ||| | | ||| || ||| ||| | |
Db      876 CTGCCTAAGGAAATGGAAGACTTTGTACAGAGCTCTGGAGAAAATGGTGTGTGGTGTGTT 935

Qy      962 ACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAAT 1021
      | |||| || |||| | | |  ||  |||| ||| | ||
Db      936 TCTCTGGGGTCAATGGTCAGTAAC---ATGACAGAAGAAAGGGCCAACGTAATTGCATCA 992

Qy     1022 GCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAA 1081
      ||| | || || | || || || ||| | |||  | | | ||| |||
Db     993 GCCCTGGCCCAGATCCCAAAAAGGTTCTGTGGA-----GATTGATGGGAATAAA 1043

Qy     1082 GATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTG 1141
      |  |  || || |||  |  |  ||| | || ||| ||||| ||
Db     1044 CCAGATACCTTAGGTCTCAATACTCGGCTCTACAAGTGGATACCCAGAATGACCTTCTA 1103

Qy     1142 GCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGCC 1201
      | ||| |||| | | | ||| | || || ||| ||| |||||
Db     1104 GGTCAATCAAAGACCAGAGCTTTTATAACTCATGGTGGAGCCAATGGCATCTACGAGGCA 1163

Qy     1202 ATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATG 1261
      || | |||| | || ||||| || || |||| || ||| |||||
Db     1164 ATCTACCATGGGATCCCTATGGTGGGGATTCCATTGTTTGCCGATCAACCTGATAACATT 1223
```

```

Qy      1262  GTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAG 1321
          | | | | | | | | | | | | | | | | | |
Db      1224  GCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTGGACTTCAACACAATGTCGAGTACA 1283

Qy      1322  ACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTG 1381
          ||| | | | | | | | | | | | | | | |
Db      1284  GACTTGCTGAATGCATTGAAGAGAGTAATTAATGATCCTTCATATAAAGAGAATGTTATG 1343

Qy      1382  GCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGG 1441
          || | | | | | | | | | | | | | |
Db      1344  AAATTATCAAGAATTCAACATGATCAACCAGTGAAGCCCCTGGATCGAGCAGTCTTCTGG 1403

Qy      1442  ATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAG 1501
          |||| | | | | | | | | | | | | | |
Db      1404  ATTGAATTTGTCATGCGCCACAAAGGAGCTAAACACCTTCGGGTTGCAGCCCACGACCTC 1463

Qy      1502  CCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGG 1547
          |||| | | | | | | | | | | | |
Db      1464  ACCTGGTTCAGTACCCTCTTTGGATGTGATTGGGTTCCCTGCTGG 1509

```

RESULT 7

US-09-356-806-7

; Sequence 7, Application US/09356806

; Patent No. 6586175

; GENERAL INFORMATION:

; APPLICANT: Penny, Laura

; APPLICANT: Galvin, Margaret

; APPLICANT: Miller, Andrew

; APPLICANT: Reidy, Michael

; TITLE OF INVENTION: Genotyping Human

; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)

and

; TITLE OF INVENTION: 2B15 (UGT2B15) Genes

; FILE REFERENCE: SEQ-22PRV2

; CURRENT APPLICATION NUMBER: US/09/356,806

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 164

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 2092

; TYPE: DNA

; ORGANISM: H. sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (38)...(1621)

US-09-356-806-7

Query Match 5.7%; Score 131.6; DB 4; Length 2092;

Best Local Similarity 49.2%; Pred. No. 6.8e-30;

Matches 470; Conservative 0; Mismatches 469; Indels 17; Gaps 4;

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Qy      593  GGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATG 652
          || || | ||| || |||| || || | || || || ||
Db      593  GGACTTCTGTTCCCTCCTTCCTATGTGCCTGTTGTTATGTCAGAACTAAGTGACCAAATG 652

Qy      653  GACTTCTGGGGCCGAGTGAAGAATTTTCT-GATGTTCTTTAGTTTCTGCAGGAGGCAACA 711

```

Db	653	ACTTTCATAGAGAGGGTAAAAAATATGATCTATGTGCTTTATTTTGAATTTTGGTTCCAA	712
Qy	712	GCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCC	771
Db	713	ATATTTGACATGAAGAAGTGGGATCAGTTCTACAGTGAAGTTCTAGGAAGACCC---AC	768
Qy	772	AGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTT	831
Db	769	TACGTTATCTGAGACAATGGCAAAGCTGACATATGGCTTATTCGAAACTACTGGGATTT	828
Qy	832	TGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACC	891
Db	829	TCAATTTCCCTCACCACCTCTTACCAAATGTTGAGTTCGTTGGAGGACTCCACTGCAAACC	888
Qy	892	TATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTT	951
Db	889	TGCCAAACCCCTACCGAAGGAAATGGAAGAGTTTGTCCAGAGCTCTGGAGAAAATGGTGT	948
Qy	952	TGTCCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGAAATCTTCAAGGA	1011
Db	949	TGTGGTGTTTTCTCTGGGGTCGATGGTCAGTAAC---ACGTCAGAAGAAAGGGCCAATGT	1005
Qy	1012	GATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCACTGTTCTCA	1071
Db	1006	AATTGCATCAGCCCTTGCCAAGATCCCAAAAAGGTTCTGTGGA-----GATTTGA	1056
Qy	1072	TTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCCTCAGAG	1131
Db	1057	TGGGAATAAACCAGATACTTTAGGACTCAATACTCGGCTGTACAAGTGGATACCCAGAA	1116
Qy	1132	TGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCACGGCGGGCAGAATAGCAT	1191
Db	1117	TGATCTTCTTGGTCACCAAAAACCAGAGCTTTTATAACTCATGGTGGAGCCAATGGCAT	1176
Qy	1192	AATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTGGAGACCAGCC	1251
Db	1177	CTATGAGGCAATCTACCATGGAATCCCTATGGTGGGCGTTCCATTGTTGCAGATCAACC	1236
Qy	1252	TGAAAACATGGTCCGAGTAGAAGCCAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCT	1311
Db	1237	TGATAACATTGCACACATGAAGGCCAAGGGAGCAGCTGTAGTTTGGACTTCCACACAAT	1296
Qy	1312	CAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTC	1371
Db	1297	GTCGAGTACAGACTTACTCAATGCACTGAAGACAGTAATTAATGATCCTTTATATAAAGA	1356
Qy	1372	CGCGGCAGTGGCTGCCAGTGTCACTCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCT	1431
Db	1357	GAATGCTATGAAATTATCAAGAATTCATCATGATCAACCAGTGAAGCCCCCTTGATCGAGC	1416
Qy	1432	GGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGT	1491
Db	1417	AGTCTTCTGGATTGAATTTGTATGCGCCATAAAGGAGCCAAGCACCTTCGGGTTGCAGC	1476
Qy	1492	CTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGG	1547

Db 1477 CCACGACCTCACCTGGTTCAGTACCACTCTTTGGATGTGACTGGGTTCTTGCTGG 1532

US-09-356-806-112

; Sequence 112, Application US/09356806

; Patent No. 6586175

; GENERAL INFORMATION:

; APPLICANT: Penny, Laura

; APPLICANT: Galvin, Margaret

; APPLICANT: Miller, Andrew

; APPLICANT: Reidy, Michael

; TITLE OF INVENTION: Genotyping Human

; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)

and

; TITLE OF INVENTION: 2B15 (UGT2B15) Genes

FILE REFERENCE: SEQ-22PRV2

; CURRENT APPLICATION NUMBER: US/09/356,806

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 164

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; SOFTWARE: FastSEQ for Windows Version 3.0
```

; SEQ ID NO 112

; LENGTH: 1976

; TYPE: DNA

; ORGANISM: H. sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (11)...(1598)

US-09-356-806-112

Query Match 5.5%; Score 128.4; DB 4; Length 1976;

Best Local Similarity 49.0%; Pred. No. 6.4e-29;

Matches 468; Conservative 0; Mismatches 471; Indels 17; Gaps 4;

Qy 593 GGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATG 652

Db 569 GGATTTCTGTTCCCTCCTTCCTATGTACCTGTTGTTATGTCAGAATTAAGTGATCAAATG 628

QY 653 GACTTCTGGGGCCGAGTGAAGAATTTTCT-GATGTTCTTTAGTTTCTGCAGGAGGCAACA 711

Db 629 ATTTTCATGGAGAGGATAAAAAATATGATACATATGCTTTATTTTGACTTTTGGTTTCAA 688

QY 712 GCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTTCACAGAAGGCTCTAGGCC 771

Db 689 ATTTATGATCTGAAGAAGTGGGACCAGTTTTATAGTGAAGTTCTAGGAAGACCCACTACA 748

QY 772 AGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTT 831

Db 749 TTATTTGAGACA---ATGGGGAAAGCTGAAATGTGGCTCATTCGAACCTATTGGGATT 804

QY 832 TGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACC 891

Db 805 TGAATTCCTCGCCATTCTTACCAAATGTTGATTTTGTGGAGGACTTCACTGTAAACC 864

Qy 892 TATTAAACCAGTACCACAAGACTTGGAGAAGTTTCATTGCCAAGTTTGGGGACTCTGGTTT 951

Db 865 AGCCAAACCCCTGCCTAAGGAAATGGAAGAGTTTGTGCAGAGCTCTGGAGAAAATGGTAT 924

Qy 952 TGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGA 1011
 ||| | | | |||| | | | | | | | | | | |||| | ||
 Db 925 TGTGGTGTCTTCTCTGGGGTCGATGATCAGTAAC---ATGTCAGAAGAAAGTGCCAACAT 981
 Qy 1012 GATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCA 1071
 ||| | | |||| | | | | | | | | | | | | | | | |
 Db 982 GATTGCATCAGCCCTTGCCAGATCCACAAAAGGTTCTATGGA-----GATTTGA 1032
 Qy 1072 TTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAG 1131
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1033 TGGCAAGAAGCCAAATACTTTAGGTTCCAATACTCGACTGTACAAGTGGTTACCCAGAA 1092
 Qy 1132 TGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCAT 1191
 ||||| | | | | | | | | | | | | | | | | | | |
 Db 1093 TGACCTTCTTGGTCATCCCAAACCAAAGCTTTTATAACTCATGGTGAACCAATGGCAT 1152
 Qy 1192 AATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCC 1251
 ||||| | | | | | | | | | | | | | | | | | | |
 Db 1153 CTATGAGGCGATCTACCATGGGATCCCTATGGTGGGCATTCCCTTGTTCGGGATCAACA 1212
 Qy 1252 TGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTCAGTTAAAGAAGCT 1311
 ||| |||| | | | | |||| | | | | | | | | | | |
 Db 1213 TGATAACATTGCTCACATGAAAGCCAAGGGAGCAGCCCTCAGTGTGGACATCAGGACCAT 1272
 Qy 1312 CAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTC 1371
 ||| | | |||| | |||| | |||| | |||| | ||||
 Db 1273 GTCAAGTAGAGATTTGCTCAATGCATTGAAGTCAGTCATTAATGACCCTGTCTATAAAGA 1332
 Qy 1372 CGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCT 1431
 | || | | | | | | | | | | | | | | | | |
 Db 1333 GAATGTCATGAAATTATCAAGAATTCATCATGACCAACCAATGAAGCCCCTGGATCGAGC 1392
 Qy 1432 GGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGT 1491
 || ||||| | | | | | | | | | | | | | | | |
 Db 1393 AGTCTTCTGGATTGAGTTTGTCTGCGCCACAAAGGAGCCAAGCACCTTCGAGTCGCAGC 1452
 Qy 1492 CTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGG 1547
 | | |||| | | | | | | | | | | | | | | | |
 Db 1453 TCACAACCTCACCTGGATCCAGTACCCTCTTTGGATGTGATAGCATTCCTGCTGG 1508

RESULT 9

US-09-813-918-1

; Sequence 1, Application US/09813918

; Patent No. 6383789

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al.

; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL001175

; CURRENT APPLICATION NUMBER: US/09/813,918

; CURRENT FILING DATE: 2001-03-22

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Human
US-09-813-918-1

Query Match 5.5%; Score 127.6; DB 4; Length 1413;
Best Local Similarity 50.1%; Pred. No. 8.9e-29;
Matches 378; Conservative 0; Mismatches 364; Indels 12; Gaps 2;

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Qy      794 AAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTT 853
      ||||| || | ||| || | || | || | || | || | || | || |
Db      551 AAAGCTGACATATGGCTTATGCGAAACCCCTGGAGTTTTCAATTTCCCTCATCCATTCTTA 610

Qy      854 CCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGAC 913
      || ||| || || ||||| || | ||||| ||||| |||| | ||
Db      611 CCAAACGTTGATTTTGTGGAGGATTCCACTGCAAACCTGCCAAACCCCTACCTAAGGAA 670

Qy      914 TTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCC 973
      ||||| || | | ||| || | ||| ||| | | | ||||| ||
Db      671 ATGGAGGAGTTTGTACAGAGCTCTGGAGAAAATGGTGTGTGGTGTCTCTGGGGTCA 730

Qy      974 ATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCAC 1033
      || | | | | | || | |||| | || | || | | || | |||
Db      731 GTGATAAGTAAC---ATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAGG 787

Qy      1034 CTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTTGGCCCAAAGATGTCCACCTG 1093
      | || ||| ||| | |||| | || | || | || | || | || |
Db      788 ATCCCAAAAAGGTTCTGTGGA-----GATTTGACGGGAATAAACAGATGCCTTA 838

Qy      1094 GCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGC 1153
      | | ||| | | ||| | || | ||| ||||| || | ||| ||||
Db      839 GGTCTCAATACTCGGCTGTACAAGTGGATACCCCAAGATGACCTTCTAGGTCATCCAAA 898

Qy      1154 ATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGT 1213
      | | | ||| | || | || | || ||||| ||||| ||| |||||
Db      899 ACCAGAGCTTTTATAACTCATGGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGG 958

Qy      1214 GTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAA 1273
      | ||||| ||||| || || | || | || | ||||| ||||| | | |
Db      959 ATCCCATGGTGGGCATTCCATTGTTTTTTGATCAACCTGATAACATTGCTCACATGAAG 1018

Qy      1274 GCCAAAAAGTTTGGTGTCTTATTCAAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTT 1333
      ||||| | |||| | | || | || | | | | || | ||
Db      1019 GCCAAGGGAGCAGCTGTTAGATTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAAT 1078

Qy      1334 AAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTC 1393
      |||| | | || | || | || | || | ||
Db      1079 GCACTGAAGACAGTAATTAATGATCCTTTATATAAAGAGAATATTATGAAATTATCAAGA 1138

Qy      1394 ATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTC 1453
      || | | || || | || || | || | || ||||| ||||
Db      1139 ATTCAACATGATCAACCAGTAAAGCCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTC 1198

Qy      1454 CTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAG 1513
      | | || || | |||| | | | | ||||| ||
Db      1199 ATGCCCCACAAAGGAGCCAAACACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAG 1258
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Qy 1514 CAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGG 1547
 | | | | | | | | | | | | | | | |
 Db 1259 TACCACTCTTTGGATGTGATTGGGTTTCTGCTGG 1292

RESULT 10

PCT-US92-00282-1

; Sequence 1, Application PC/TUS9200282
 ; GENERAL INFORMATION:
 ; APPLICANT: OWENS, IDA S.
 ; APPLICANT: RITTER, JOSEPH K.
 ; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
 ; TITLE OF INVENTION: THEREIN.
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 ; STREET: 1615 L STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20036-5601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/00282
 ; FILING DATE: 19920110
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SCOTT, WATSON T.
 ; REGISTRATION NUMBER: 26581
 ; REFERENCE/DOCKET NUMBER: 91532-PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; TELEX: 6714627 CUSH
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2336 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 PCT-US92-00282-1

Query Match 5.1%; Score 118; DB 5; Length 2336;
 Best Local Similarity 47.6%; Pred. No. 1.2e-25;
 Matches 457; Conservative 0; Mismatches 485; Indels 18; Gaps 3;

Qy 599 CCAATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTC 658
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 Db 559 CCCAACCATTCTCTACGTGCCAGGCCCTCTCTCTCTCATTGAGATCACATGACCTTC 618
 Qy 659 TGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATG 718

Db	619	CTGCAGCGGGTGAAGAACATGCTCATTGCCTTTTCACAGAACTTTCTGTGCGACGTGGTT	678
Qy	719	CAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTG	778
Db	679	TATTCCTCCCGTATGCAACCCTTGCCCTCAGAATTCCTTCAGAGAG-----AGGTGACTGTC	732
Qy	779	TCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTT	838
Db	733	CAGGACCTATTGAGCTCTGCATCTGTCTGGCTGTTTAGAAGTGACTTTGTGAAGGATTAC	792
Qy	839	GCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAA	898
Db	793	CCTAGGCCCATCATGCCCAATATGGTTTTTGTGGTGGGAATCAACTGCCTTCACCAAAAT	852
Qy	899	CCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTT	958
Db	853	CCACTATCCCAGGAATTTGAAGCCTACATTAATGCTTCTGGAGAACATGGAATTGTGGTT	912
Qy	959	GTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAAC	1018
Db	913	TTCTCTTTGGGATCAATGGTCTCAGAAATTCAGAAA---GAAGAAAGCTATGGCAATTGCT	969
Qy	1019	AATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCC	1078
Db	970	GATGCTTTGGGCAAAATCCCTCAGACAGTCCTGTGGCGGTACACTGGAACCCGACCATCG	1029
Qy	1079	AAAGATGTCCACCTGGCTGCAAATGTGAAAATGTGGACTGGCTTCCTCAGAGTGACCTC	1138
Db	1030	AATCTTGCGAAC-----AACACGATACTTGTTAAGTGGCTACCCCAAACGATCTG	1080
Qy	1139	CTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAG	1198
Db	1081	CTTGGTCACCCGATGACCCGTGCCTTTATCACCCATGCTGGTTCCCATGGTGTATTATGAA	1140
Qy	1199	GCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAAC	1258
Db	1141	AGCATATGCAATGGCGTTCCCATGGTGATGATGCCCTTGTTTGGTGATCAGATGGACAAT	1200
Qy	1259	ATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCA	1318
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Qy	1319	GAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCA	1378
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Qy	1379	GTGGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGTGGTGGGC	1438
Db	1321	AGGCGCCTCTCCAGCCTTCACAAGGACCGCCCGGTGGAGCCGCTGGACCTGGCCGTGTTT	1380
Qy	1439	TGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAG	1498
Db	1381	TGGGTGGAGTTTGTGATGAGGCACAAGGGCGCGCCACACCTGCGCCCCGAGCCCACGAC	1440
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Db 1441 CTCACCTGGTACCAGTACCATTCCTTGGACGTGATTGGTTTCCTCTTGGCCGTCGTGCTG 1500

RESULT 11

PCT-US92-00282-2

; Sequence 2, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00282

; FILING DATE: 19920110

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: SCOTT, WATSON T.

; REGISTRATION NUMBER: 26581

; REFERENCE/DOCKET NUMBER: 91532-PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; TELEX: 6714627 CUSH

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2339 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

PCT-US92-00282-2

Query Match 4.8%; Score 111.2; DB 5; Length 2339;

Best Local Similarity 48.5%; Pred. No. 1.5e-23;

Matches 376; Conservative 0; Mismatches 388; Indels 12; Gaps 2;

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Db      740 ATCTTGTGTCAGCTATGCATCCGTGTGGCTGTCCGAGGGGACTTTGTGATGGACTACCCCA 799

Qy      843 GACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGAAAAACCTATTAAACCAG 902
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Db      800 GGCCGATCATGCCCAACATGGTCTTCATTGGGGGCATCAACTGTGCCAACGGGAAGCCAC 859
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; PRIOR APPLICATION NUMBER: 60/084,807
 ; PRIOR FILING DATE: 1998-05-07
 ; NUMBER OF SEQ ID NOS: 124
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 17
 ; LENGTH: 735
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(735)
 US-09-305-856B-17

Query Match 4.1%; Score 95.6; DB 4; Length 735;
 Best Local Similarity 50.2%; Pred. No. 4.5e-19;
 Matches 236; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Qy	1149	CAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGC	1208
Db	227	CGATGACCCGTGCCTTTATCACCCATGCTGGTTCCCATGGTGTCTTATGAAAGCATATGCA	286
Qy	1209	ATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAG	1268
Db	287	ATGGCGTTCCCATGGTGTATGATGCCCTTGTTTGGTGATCAGATGGACAATGCAAAGCGCA	346
Qy	1269	TAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGAGACATTGG	1328
Db	347	TGGAGACTAAGGGAGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCTGAAGATTTAG	406
Qy	1329	CTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCA	1388
Db	407	AAAATGCTCTAAAAGCAGTCATCAATGACAAAAGTTACAAGGAGAACATCATGCGCCTCT	466
Qy	1389	GTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACC	1448
Db	467	CCAGCCTTCACAAGGACCGCCCGGTGGAGCCGCTGGACCTGGCCGTGTTCTGGGTGGAGT	526
Qy	1449	ACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGC	1508
Db	527	TTGTGATGAGGCACAAGGGCGCGCCACACCTGCGCCCCGAGCCACGACCTCACCTGGT	586
Qy	1509	ATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTG	1558
Db	587	ACCAGTACCATTCTTGGACGTGATTGGTTTCCTCTTGGCCGTCGTGCTG	636

RESULT 13

US-08-232-463-14
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.

| | | | | |

US-09-356-806-5

; Sequence 5, Application US/09356806

; Patent No. 6586175

; GENERAL INFORMATION:

; APPLICANT: Penny, Laura

; APPLICANT: Galvin, Margaret

; APPLICANT: Miller, Andrew

; APPLICANT: Reidy, Michael

; TITLE OF INVENTION: Genotyping Human

; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)

and

; TITLE OF INVENTION: 2B15 (UGT2B15) Genes

; FILE REFERENCE: SEQ-22PRV2

; CURRENT APPLICATION NUMBER: US/09/356,806

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEO ID NOS: 164

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; SOFTWARE: FastSEO for Windows Version 3.0
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; SEO ID NO 5

; LENGTH: 689

; TYPE: DNA

; ORGANISM: H. sapiens

; FEATURE:

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; NAME/KEY: Other
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;  LOCATION:  (123) ... (342)
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US-09-356-806-5

Query Match 2.8%; Score 63.8; DB 4; Length 689;

Best Local Similarity 60.8%; Pred. No. 3e-09;

Matches 104; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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Db 117 TCCTAGGTCACCCAAAAACCAGAGCTTTTATAACTCATGGTGGAGCCAATGGCATCTATG 176

Ov 1197 AGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAA 1256

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Ov 1257 ACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGA 1307

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Db 237 ACATTGCACACATGAAGGCCAAGGGAGCAGCTGTTAGTTTGGACTTCCACA 287

Search completed: May 16, 2004, 14:05:18

Job time : 194 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 07:14:19 ; Search time 1397 Seconds
(without alignments)
7536.345 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 aggggtcccttagccgggcgcc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match	Length	DB	ID	Description
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4	2320	100.0	2320	13	US-10-013-907A-281	Sequence 281, App
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ALIGNMENTS

RESULT 1
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 ; Sequence 281, Application US/09946374
 ; Publication No. US20030073129A1
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
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; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
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Query Match          100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
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Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCTTTCTGGA 360
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Db    301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
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Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
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Db	421	GTTGCAGTGCAGTCATTTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
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Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
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Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260

Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAAGTTAAAGAAGCTCAAGGCAGA	1320
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Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTTCTGGCAGCCCCATTCTCTAGTCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTTCTGGCAGCCCCATTCTCTAGTCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100

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Qy      2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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Db      2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160

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Db      2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220

Qy      2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
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Qy      2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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RESULT 2

US-10-015-395A-281

; Sequence 281, Application US/10015395A

; Publication No. US20040073015A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C57

; CURRENT APPLICATION NUMBER: US/10/015,395A

; CURRENT FILING DATE: 2001-12-12

; Prior application removed - See file Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 281

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-015-395A-281

Query Match 100.0%; Score 2320; DB 12; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
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Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGATTTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGATTTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAAC TTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAAC TTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960

Db	901	 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	 GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	 GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	 GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800

Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 3

US-10-006-485A-281

; Sequence 281, Application US/10006485A

; Publication No. US20030064062A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
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; PRIOR FILING DATE: 1998-09-02
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; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 2320; DB 13; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
      |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
      |||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
      |||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
      |||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTTCTTTCTGGA 360
      |||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
      |||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
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Db    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

Qy    481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
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Db    481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
      |||
Db    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
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Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
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Qy	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440

Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
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RESULT 4

US-10-013-907A-281

; Sequence 281, Application US/10013907A

; Publication No. US20030064925A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C34

; CURRENT APPLICATION NUMBER: US/10/013,907A

; CURRENT FILING DATE: 2001-12-10

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 281

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-013-907A-281

Query Match 100.0%; Score 2320; DB 13; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
|
Db 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
|
Db 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
|
Db 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy 241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
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Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTTCGGCTCTTGGAAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTTCGGCTCTTGGAAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140

Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980

Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 5

US-10-015-499A-281

; Sequence 281, Application US/10015499A

; Publication No. US20030065142A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C42

; CURRENT APPLICATION NUMBER: US/10/015,499A

; CURRENT FILING DATE: 2001-12-11

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 281

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-015-499A-281

Query Match 100.0%; Score 2320; DB 13; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60
      |||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
      |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
      |||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
      |||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
      |||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
      |||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
      |||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTTAAAGAATGAGAA 480
      |||
Db    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTTAAAGAATGAGAA 480

Qy    481 CTTGCACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
      |||
Db    481 CTTGCACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600
      |||
Db    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600

Qy    601 AATCCCCTTGCTTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660
      |||
Db    601 AATCCCCTTGCTTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG 660

Qy    661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
      |||
Db    661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720

Qy    721 GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC 780
      |||
Db    721 GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC 780
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Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAAATCCGAAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAAATCCGAAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680

Db	1621		AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681		TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681		TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741		TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741		TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801		ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801		ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861		CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861		CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921		TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921		TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981		CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981		CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041		TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCACT	2100
Db	2041		TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCACT	2100
Qy	2101		TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101		TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161		AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161		AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221		CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221		CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281		AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281		AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 6

US-10-226-254A-281

; Sequence 281, Application US/10226254A

; Publication No. US20030224478A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

```

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C68
; CURRENT APPLICATION NUMBER: US/10/226,254A
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 281
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-226-254A-281

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Query Match          100.0%; Score 2320; DB 13; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
        |||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
        |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCTTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCTTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020

Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860

Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 7

US-10-006-856A-281

; Sequence 281, Application US/10006856A

; Publication No. US20030044841A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C14

; CURRENT APPLICATION NUMBER: US/10/006,856A

; CURRENT FILING DATE: 2002-05-10

; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 281
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-856A-281

Query Match 100.0%; Score 2320; DB 15; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCACTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTTGCACTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

Qy    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCTTTCCTGATTGCTGAGAAGCT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCTTTCCTGATTGCTGAGAAGCT 540

Qy    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600

Qy    601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 660

Qy    661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
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Db	661		GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Db	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381		GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381		GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441		GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441		GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501		GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560

Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

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; Sequence 281, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 281
;   LENGTH: 2320
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-006-818A-281

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Query Match          100.0%;  Score 2320;  DB 15;  Length 2320;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 2320;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360

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Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200

Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100

Db	2041		TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101		TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101		TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161		AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161		AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221		CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Db	2221		CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAA	2280
Qy	2281		AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281		AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 9

US-10-015-393A-281

; Sequence 281, Application US/10015393A

; Publication No. US20030069179A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C46

; CURRENT APPLICATION NUMBER: US/10/015,393A

; CURRENT FILING DATE: 2002-06-10

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 281

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-015-393A-281

Query Match 100.0%; Score 2320; DB 15; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900

Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740

Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 10

US-10-015-869A-281

; Sequence 281, Application US/10015869A

; Publication No. US20030073130A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 281
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-281
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Query Match          100.0%; Score 2320; DB 15; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60
        |||
Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGA 60

Qy     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
        |||
Db     61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
        |||
Db    121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
        |||
Db    181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
        |||
Db    241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGATTTCTTTCTGGA 360
        |||
Db    301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGATTTCTTTCTGGA 360

Qy    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420
        |||
Db    361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC 420

Qy    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
        |||
Db    421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

Qy    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
        |||
Db    481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
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Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAGTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAGTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTGATCCTGCGCTCCCAACCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440

Db	1381	 GGCTGCCAGTGTCTATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	 GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	 GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	 CTTGTCTCCTTTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	 TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280

Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 11

US-10-012-121A-281

; Sequence 281, Application US/10012121A

; Publication No. US20030073810A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

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; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C20

; CURRENT APPLICATION NUMBER: US/10/012,121A

; CURRENT FILING DATE: 2001-12-07

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 281

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-012-121A-281

Query Match 100.0%; Score 2320; DB 15; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
|||||
Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
|||||
Db 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
|||||
Db 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACCATGCTTAACCA 240
|||||

Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCCAA	1080

Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Qy	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920

Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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 Db 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
 ||||||||||||||||||
 Qy 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
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 Db 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
 ||||||||||||||||||
 Qy 2041 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT 2100
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 Db 2041 TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAGT 2100
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 Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
 ||||||||||||||||||
 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
 ||||||||||||||||||
 Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
 ||||||||||||||||||
 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
 ||||||||||||||||||
 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
 ||||||||||||||||||
 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
 ||||||||||||||||||
 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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RESULT 12

US-10-006-116A-281

; Sequence 281, Application US/10006116A

; Publication No. US20030082626A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C15

; CURRENT APPLICATION NUMBER: US/10/006,116A

; CURRENT FILING DATE: 2001-12-16

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
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; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882

; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 2320; DB 15; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780

Db	721		GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781		TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841		TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901		AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961		GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Db	1021		TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCCAA	1080
Qy	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081		AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141		GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201		CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261		GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321		GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381		GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381		GGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441		GATTGACCACGTCCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCTAGCA	1500
Db	1441		GATTGACCACGTCCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCTAGCA	1500
Qy	1501		GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501		GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561		GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620

Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTTGTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320
Db	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

RESULT 13

US-10-006-117A-281

; Sequence 281, Application US/10006117A

; Publication No. US20030082627A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

```

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C13
; CURRENT APPLICATION NUMBER: US/10/006,117A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 281
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-117A-281

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Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAAATGTGAAAATGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAAATGTGAAAATGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260

Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGCGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGCGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100

Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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 Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
 |||
 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
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 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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RESULT 14

US-10-017-527A-281

; Sequence 281, Application US/10017527A

; Publication No. US20030082628A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

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; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C63

; CURRENT APPLICATION NUMBER: US/10/017,527A

; CURRENT FILING DATE: 2001-12-13

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098749

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098750

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098803

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098821

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098843

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/099536

; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-09
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; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06

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; PRIOR APPLICATION NUMBER: 60/104987
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; PRIOR APPLICATION NUMBER: 60/105002
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; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

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Query Match          100.0%; Score 2320; DB 15; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAGAGGTCCTTTTATGCCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	241	CAAAGAGGTCCTTTTATGCCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960

Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTGAGTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTGAGTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800

Db 1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1800
 Qy 1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860
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 Db 1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860
 Qy 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
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 Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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 Qy 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
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 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
 Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 15

US-10-013-913A-281

; Sequence 281, Application US/10013913A

; Publication No. US20030083462A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C40
; CURRENT APPLICATION NUMBER: US/10/013,913A
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 281
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-013-913A-281

Query Match 100.0%; Score 2320; DB 15; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Qy	61	AGTGAGCATGGCTGGGCGAGAGTGTCTTCTTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCGAGAGTGTCTTCTTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Db	301	TTGGCTTGACCTGAAGATCATCAAAGAGAAATTTAAAAAGAGTTTGGATTCTTTCTGGA	360
Qy	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600

Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAAGTTTATTGTTGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAAGTTTATTGTTGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440

Qy	1441	GATTGACCACGTCTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Qy	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Db	2041	TGCCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
Qy	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2101	TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA	2280
Db	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA	2280
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA	2320

|||||
Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

Search completed: May 16, 2004, 14:28:50
Job time : 1403 secs